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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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seq length: 0 seq length: 2000000000
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/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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US-09-1188-930-305

US-09-118-930-305

US-09-312-283C-305

US-08-303-238-1

US-08-458-834-1

US-08-458-834-7

US-09-540-245A-7

US-09-540-153-7
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US-08-442-063A-45

US-08-442-063A-42

US-08-303-238-3

US-08-458-834-3

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     Sequence 48, Appl
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Sequence 47, Appl
Sequence 3, Appli
Sequence 3, Appli
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Sequence 39, Appl
Sequence 39, Appl
Sequence 39, Appl
Sequence 30, Appl
Sequence 30, Appl
Sequence 305, Appl
Sequence 105, Appl
Sequence 1, Appli
Sequence 7, Appli
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Sequence 4, Appli
Sequence 4, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 3, Appli
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273	273	273	273	278	280	281.5	291	295.5	295.5	302	303.5	314.5	314.5	317	317	317	320
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US-08-473-089-49	US-08-477-346-49	US-09-063-950-5	US-08-190-802A-49	US-08-986-485-2	US-08-442-063A-57	US-09-482-273-105	US-08-986-485-5	US-09-170-496D-278	US-09-170-496D-264	US-09-996-243-501	US-09-996-243-229	US-08-458-834-2	US-08-303-238-2	US-09-540-153-2	US-09-540-245A-2	US-09-191-647-2	US-09-182-024A-2
Sequence 49, Appl	Sequence 49, Appl	Sequence 5, Appli	Sequence 49, Appl	Sequence 2, Appli	Sequence 57, Appl	Sequence 105, App	Sequence 5, Appli	•	Sequence 264, App	Sequence 501, App	Sequence 229, App	Sequence 2, Appli					

ALIGNMENTS

## ; SEQUENCE CHARACTERISTICS: ; LENGTH: 33 amino acids ; TYPE: amino acid ; TOPOLOGY: linear ; MOLECULE TYPE: protein US-08-442-063A-27 RESULT 1 US-08-442-063A-27 Sequence 27, Application Patent No. 5705609 GENERAL INFORMATION: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentlIn Release #1.0, Version #1 CURRENT APPLICATION NATA: APPLICATION NUMBER: US/08/442,063A FILING DATE: 16-MAY-1995 CLASSIFICATION DATA: APPLICATION NUMBER: US 07/865,652 APPLICATION NUMBER: US 07/865,652 APPLICATION NUMBER: US 07/865,652 APPLICATION NUMBER: US 07/865,652 ATTORNEY/AGENT INFORMATION: NAME: CAMPBELL, CATHEYN A. REGISTRATION NUMBER: 31,815 REFERENCE/DOCKET NUMBER: P-LA 1454 TELECOMMUNICATION INFORMATION: TELEPHONE: 619-535-900 TELEFAX: 619-535-8949 INFORMATION FOR SEQ ID NO: APPLICANT: RUOSLAHTI, ERKKI I. APPLICANT: PIERSCHBACHER, MICHAEL D. APPLICANT: CARDENAS, JOSE APPLICANT: CARDENAS, JOSE APPLICANT: CRAIG, WILLIAM APPLICANT: MULLEN, DANIEL G. APPLICANT: MULLEN, DANIEL G. TITLE OF INVENTION: INCIDENTING CELL REGULATORY FACTORS NUMBER OF SEQUENCES: 6: CORRESPONDENCE ADDRESS: ADDRESSEE: CAMPBELL AND FLORES STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE CITY: SAN DIEGO COUNTRY: UNITED STATES CALIFORNIA 619-535-9001 US/08442063A #1.25

Query Match Best Local Similarity Matches 328; Conserv

Conservative

99.8%; Score 1709; DB 1; 100.0%; Pred. No. 4.6e-158; tive 0; Mismatches 0;

Length 333;

0;

Gaps

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; MOLECULE TYPE: US-08-303-238-4
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                              TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 5654270
GENERAL INFORMATION:
APPLICANT: RUOSLA
                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, VS
CURRENT APPLICATION DATA;
APPLICATION NUMBER: US/08/303,238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                            REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: P-J
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-335-9001
                                                                                                                                                                                                                APPLICANT: PIERSCHBACHER, MICHAEL D.

APPLICANT: BORDER, WAYNE A.

TITLE OF INVENTION: INHIBITORS OF CELL REGULATORY FACTORS

TITLE OF INVENTION: AND METHODS FOR PREVENTING OR REDUCING SCARRING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE
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                                                                                                                                                                                                     NAME: KONSKI, ANTOINETTE F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: SAN DIEGO
STATE: CALIFORNI
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LONGAKER, MICHAEL T.
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APPLICANT: RUOSLAH
APPLICANT: LONGAKE
APPLICANT: WHITBY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08458834 Patent No. 6277812
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Best Local
           TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                               FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978
FILING DATE: 17-NOV-1992
ATTORNEY_AGENT INFORMATION:
NAME: KONSKI, ANTOINETTE F.
REGISTRATION NUMBER: 202
REFERENCE/DOCKET NUMBER: P-LA
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: WHITEY, DAVID J.

APPLICANT: HARPER, JOHN R.

APPLICANT: PIERSCHBACHER, MICHAEL D.

APPLICANT: BORDER, WAYNE A.

TITLE OF INVENTION: INHIBITORS OF CELL REGULATORY FACTORS
TITLE OF INVENTION: AND METHODS FOR PREVENTING OR REDUCING
NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
ZIP: 921
                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                        SSEE: CAMPBELL AND FLORES
I: 4370 LA JOLLA VILLAGE |
SAN DIEGO
CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NPVQYWEIQPSTFRCVYVRSAIQLGNYK 329
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359 amino acids
                                                619-535-8949
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LONGAKER, MICHAEL
                                                                    619-535-9001
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MICHAEL T
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-458-834-4
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US-08-272-919-2
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APPLICANT: Craig,
APPLICANT: Harper,
APPLICANT: Hernande
APPLICANT: Kostel,
APPLICANT: Parker,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 328;
                                              APPLICATION NUMBER: US/08/272,91
FILING DATE: 08-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 91,815
REFERENCE/DOCKET NUMBER: P-LA 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
              TELEFAX: (619) 535-8949 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Kostel, Paul J.
APPLICANT: Parker, Jonathan R.
APPLICANT: Vedvick, Thomas S.
TITLE OF INVENTION: Processes for the Purification of Human
TITLE OF INVENTION: Recombinant Decorin and the Detection of Guanidinium
NUMBER OF SEQUENCES: 2
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STATE: (
COUNTRY:
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CHARACTERISTICS:
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4370 La Jolla Village Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craig, William S.
Harper, John R.
Hernandez, Sam D.
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-272-919-2
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Best Local Similarity 100.
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Patent No.
                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: THM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, V
CURRENT APPLICATION DATA;
APPLICATION NUMBER: US/08/619,916
                      FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/2
PILING DATE: 08-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-
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CORRESPONDENCE ADDRESS:
Campbell and Flores
The Total Control of the Control
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TITLE OF INVENTION: Processes for the Purification of Human
TITLE OF INVENTION: Recombinant Decorin and the Detection o
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APPLICANT: Vedvick,
TELECOMMUNICATION INFORMATION:
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CITY: San Diego
STATE: California
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No. 576327
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Harper, John R.
Hernandez, Sam D.
Kostel, Paul J.
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Pred. No. 1.5e-157;
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PCT-US95-08542-2
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/
FILING DATE: 07-UUL-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: PERKINS, SUBBAN M.
REGISTRATION NUMBER: 36,405
REFERENCE/DOCKET NUMBER: FP-L
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (619) 535-894
INFORMATION FOR SEQ ID NO:
, SEQUENCE CHARACTERISTICS:
   TELEFAX: (
                                                                                                                                                                                                       ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: La Jolla Cancer Research Foundation
TITLE OF INVENTION: Processes for the Purification
TITLE OF INVENTION: Human
TITLE OF INVENTION: Recombinant Decorin and the Det
NUMBER OF SEQUENCES: 2
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Local Similarity 100.0%; Pred. No. 1.5e-157;
108 327; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                          ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village |
CITY: San Diego
STATE: California
COUNTR: USA
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ID NO: 2:
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                                                                                                                                                                         PCT/US95/08542
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APPLICANT: TERMINE, JOHN D.; YOUNG, ME; ROBEY, PAMELA G.

TITLE OF INVENTION: CDNA SEQUENCES OF NUMBER OF SEQUENCES: 13

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/432,044

FILING DATE: 03-NOV-1989
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                                                                                                                                                                                                                                                                                                           Query Match
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TYPE: amino acid
TOPOLOGY: linear
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Similarity 97.3%;
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                RELHLDNNKLTRVPGGLAEHKYIQVVYLHNNNISVVGSSDFCPPGHNTKKASYSGVSLFS 301
                                                                                                                LQELRAHENEITKVRKVTFNGLNQMIVIELGTNPLKSSGIENGAFQGMKKLSYIRIADTN
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                                                                                                                                                                          KITEIKOGDFKNLKNLHALILVNNKISKVSPGAFTPLVKLERLYLSKNQLKELPEKMPKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ITSIPQGLPPSLTELHLDGNKISRVDAASLKGLNNLAKLGLSFNSISAVDNGSLANTPHL 241
RELHLDNNKLTRVPGGLAEHKYIQVVYLHNNNISVVGSSDFCPPGHNTKKASYSGVSLFS
                                                          ITKVRKVTFNGLTELHLDGNKISRVDAASLKGLNNLAKLGLSFNSISAVDNGSLANTPHL
                                                                         ITSIPQGLPPSLTELHLDGNKISRVDAASLKGLNNLAKLGLSFNSISAVDNGSLANTPHL
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100.0%; Pr
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                                                                                                                                                                                                                                                                                          Score 1653; DB 6;
Pred. No. 1.4e-152;
2; Mismatches 7;
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Pred. No. 1.5e-157;
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Best Local 9
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/442,063A
FILING DATE: 16-MAY-1995
CLASIFICATION: 514
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/865,652
FILING DATE: 03-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 1454
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
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                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: CEAIG, WILLIAM
APPLICANT: MULLEN, DANIEL G.
TITLE OF INVENTION: DECORIN FRAGMENTS AND METHODS OF
TITLE OF INVENTION: INHIBITING CELL REGULATORY FACTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Dalas
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5705609
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CALIFORNIA
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                 ITSIPQGLPPSLTELHLDGNKISRVDAASLKGLNNLAKLGLSFNSISAVDNGSLANTPHL 241
                                                                                       LQELRAHENEITKVRKVTFNGLNQMIVIELGTNPLKSSGIENGAFQGMKKLSYIRIADTN
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ITSIPQGLPPSLTELHLDGNKISRVDAASLKGLNNLAKLGLSFNSISAVDNGSLANTPHL
                                                                  LQELRAHENEITKVRKVTFNGLNQMIVIELGTNPLKSSGIENGAFQGMKKLSYIRIADTN
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4370 LA JOLLA VILLAGE DRIVE, SUITE 700
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                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                             protein
                                                                                                                                                                                                                                                                                         91.5%; Score 1567; DB 1; 1
100.0%; Pred. No. 2.7e-144;
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COMPUTER: IBM PC COMPATING
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
SOFTWARE: PATENTIN PATA:
APPLICATION NATA:
APPLICATION NUMBER: US/08/442,063A
FILING DATE: 16-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/865,652
FILING DATE: 03-APR-1992
FILING DATE: 03-APR-1992
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Patent No. 5705609
GENERAL INFORMATION:
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Best Local Similarity 100.0%; Pred. No. 2.6e-131;
Matches 278; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 03-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL CAMPROVA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 282 amino acid
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TITLE OF INVENTION: DECORIN FRAGMENTS AND METHODS OF
TITLE OF INVENTION: INHIBITING CELL REGULATORY FACTORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: CAMPBELL, CATHRYN A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 1454
                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid TOPOLOGY: linear
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STATE: CALIFORNIA
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182 ITSIPQGLPPSLTELHLDGNKISRVDAASLKGLNNLAKLGLSFNSISAVDNGSLANTPHL 241
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                                                               LQELRAHENBITKVRKVTFNGLNQMIVIBLGTNPLKSSGIENGAFQGMKKLSYIRIADTN 181
                                     LQELRAHENEITKVRKVTFNGLNQMIVIELGTNPLKSSGIENGAFQGMKKLSYIRIADTN
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PIERSCHBACHER,
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HER, MICHAEL
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US-08-442-063A-42
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                                                                                                                                                                                                       Matches 231;
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                                                                                                                                                                                                                                                                                                                      TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 0
FILING DATE: 03-APR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 619-535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                       NAME: CAMPBELL, CATHRYN A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 1454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 16-MA
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                                                                                                                                                                                                                                                                                                               ENGTH:
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5. 5705609
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                                                                                                                                                                                                                                                                                               amino acid
| TSIPQGLPBLTELHLDGNKISRVDAASLKGLNNLAKLGLSFNSISAVDN 232
                                                                                          KITEIKDGDFKNLKNLHALILVNNKISKVSPGAFTPLVKLERLYLSKNQLKELPEKMPKT
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                                         LQELRAHENEITKVRKVTFNGLNQMIVIELGTNPLKSSGIENGAFQGMKKLSYIRIADTN
                                                                   LOELRAHENEITKVRKVTFNGLNOMIVIELGTNPLKSSGIENGAFOGMKKLSYIRIADTN
                                                                                                                                               EASGIGPEVPDDRDFEPSLGPVCPFRCQCHLRVVQCSDLGLDKVPKDLPPDTTLLDLQNN
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                                                                                                                                                                                                                                                                                                             236 amino acids
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VENTION: DECORIN FRAGMENTS AND METHODS OF
VENTION: INHIBITING CELL REGULATORY FACTORS
                                                                                                                                                                                                       Conservative
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100.0%; Pro
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                                                                                                                                                                                                                Score 1186; DB 1; Pred. No. 2.1e-107;
                                                                                                                                                                                                      Mismatches
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US-08-303-238-3
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                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                             LENGTH:
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            241
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Query Match 56.4%;
Best Local Similarity 56.5%;
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PRIOR APPLICATION NUMBER: US 07
APPLICATION NUMBER: US 07
PTILING DATE: 17-NOV-1992
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REFERENCE/DOCKET NUMBER: P-
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: HM PC compatible
COMPUTER: HM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ATTORNEY/AGENT INFORMATION:
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                                                                219 KLTGIPKOLPETLNELHLDHNKIQAIELEDLLRYSKLYRLGLGHNQIRMIENGSLSFLPT
                                                                                                                                              160 SLVELRIHDNRIRKVPNGVFSGLRNYNCIEMGGNPLENSGFEPGAFDGL-KLNYLRISEA 218
                                                                                                     181 NITSIPOGLPPSLTBLHLDGNKISRVDAASLKGLNNLAKLGLSFNSISAVDNGSLANTPH
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LRELHLDNNKLTRVPGGLAEHKYIQVVYLHNNNISVVGSSDFCPPGHNTKKASYSGVSLF 300
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UNITED STATES
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4370 LA JOLLA VILLAGE
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PIERSCHBACHER, MICHAEL D.
BORDER, WAYNE A.
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LONGAKER, MICHAEL T.
WHITBY, DAVID J.
                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Pred. No. le-85;
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US-08-458-834-3
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; MOLECULE TYPE: protein
US-08-458-834-3
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Best Local :
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INFORMATION FOR SEQ ID NO: 3:
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APPLICANT:
APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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APPLICANT: BORDER, WAYNE A.
TITLE OF INVENTION: INHIBITORS OF CELL REGULATORY FACTORS
TITLE OF INVENTION: AND METHODS FOR PREVENTING OR REDUCING SCARRING
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: KONSKI, ANTOINETTE F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: P-LA
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APPLICATION NUMBER: US 0
FILING DATE: 17-NOV-1992
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                             Local Similarity 56.4%; Score 966; DB 3; Length 368; Local Similarity 56.5%; Pred. No. 1e-85; res 186; Conservative 51; Mismatches and Transles
                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
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STATE: CALIFORNIA
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                                                                                                                                     NKITEIKDGDFKNLKNLHALILVNNKISKVSPGAFTPLVKLERLYLSKNQLKELPEKMPK 120
                                                                                                           NDISELRKDDFKGLQHLYALVLVNNKISKIHEKAFSPLRNVQKLYISKNHLVEIPPNLPS
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                                             SLVELRIHDNRIRKVPNGVFSGLRNMNCIEMGGNPLENSGFEPGAFDGL-KLNYLRISEA
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LONGAKER, MICHAEL T.
WHITBY, DAVID J.
HARPER, JOHN R.
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5340934-2
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US-08-442-063A-39
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Matches
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APPLICANT: TER
ROBEY, PAMELA G.
                                                                                                                                                                                                                   Patent No. 5705609
GENERAL INFORMATION:
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Best Local Similarity
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                                CITY:
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                                                             ADDRESSEE:
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FILING DATE: 03-NOV-1989
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/432,044
241 LRELHLDNNKLTRVPGGLAEHKYIQVVYLHNNNISVVGSSDFCPPGHNTKKASYSGVSLF 300
                                                                                                                                                                                          219 KLTGIPKOLPETLNELHLÖHNKIQAIELEDLLRYSKLYRLGLGHNQIRMIENGSLSFLPT
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                                                                                                LRELHLDNNKLARVPSGLPDLKLLQVVYLHSNNITKVGVNDFCPMGFGVKRAYYNGISLF
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Pred. No. 1.3e-85;
3; Mismatches 89
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APPLICANT: MULLEN, DANIEL G.
TITLE OF INVENTION: DECORIN FRAGMENTS AND METHODS
TITLE OF INVENTION: INHIBITING CELL REGULATORY FAC
NUMBER OF SEQUENCES: 62 CORRESPONDENCE ADDRESS: SAN DIEGO CALIFORNIA Application US/08442063A 3: CAMPBELL AND FLORES
4370 LA JOLLA VILLAGE PIERSCHBACHER, MICHAEL CARDENAS, JOSE CRAIG, WILLIAM UNITED STATES RUOSLAHTI, ERKKI I. DRIVE, ū SUITE

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RESULT 15
US-09-724-864-43
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                                                      ; ORGANISM: Mouse US-09-724-864-43
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                                                                                                                                                                                                                                                                                                                                          Sequence 43, Application Patent No. 6380362 GENERAL INFORMATION:
                                                                                                                           SOFTWARE:
SEQ ID NO 43
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Query Match
Best Local Similarity
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APPLICATION NUMBER: US 07/865,652

FILING DATE: 03-APR-1992

ATTORNEY/AGENT INFORMATION:

NAME: CAMPBELL, CATHRYN A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-LA 1454

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/724,864
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 72
                                                                                                                                                                                                                                                   APPLICANT: Murison, James G.
TITLE OF INVENTION: Polymucleotides, polymeptides expressed
TITLE OF INVENTION: by the polymucleotides and methods for their use.
FILE REFERENCE: 11000.1050U1
                                                                                                                                                                                                                                                                                                          APPLICANT: Watson, James D
APPLICANT: Murison, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 619-535-8949 INFORMATION FOR SEQ ID NO: 39:
                                                                                          TYPE: PRT
                                                                                                          LENGTH:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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les 183; Conserv
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
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                                                                                                                                            FastSEQ for Windows Version 4.0
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 54.0%;
53.7%;
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Score 925.5; DB 4;
Pred. No. 9.3e-82;
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                Length 373;
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RESULT 16
US-08-442-063A-36
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US-08-442-063A-36
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                                                                                                                                                                                       CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/865,652
FILING DATE: 03-APR-1992
ATTORNEY,AGENT INFORMATION:
NAME: CAMPBELL, CATHEYN A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 1454
                                                                                        TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: RUOSLA
APPLICANT: PIERSC
                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,06:
FILING DATE: 16-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: CAMPBELL AND FLORES
                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 619-535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: DECORIN FRAGMENTS AND METHODS OF TITLE OF INVENTION: INHIBITING CELL REGULATORY FACTORS NUMBER OF SEQUENCES: 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                   TYPE: amino acid
TOPOLOGY: linear
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                                                                            LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 RAHENEITKVRKVTFNGLNOMIVIELGTNPLKSSGIENGAFOGMKKLSYIRIADTNITSI
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SAN DIEGO
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WENTION: DECORIN FRAGMENTS AND METHODS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RUOSLAHTI, ERKKI I.
PIERSCHBACHER, MICHAEL
CARDENAS, JOSE
CRAIG, WILLIAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UNITED STATES
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Length 141;

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                                                                                                                             US-08-442-063A-33
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Best Local Similarity
Matches 136; Conserv
                                                                Matches
                                                                               Best
                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, VGCURRENT APPLICATION DATA:
APPLICATION UMMBER: US/08/442,063A
FILING DATE: 16-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/865,652
APPLICATION OBTA:
APPLICATION NUMBER: US 07/865,652
APTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, CATHRYN A.
REGISTRATION NUMBER: 31,815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: RUOSLA
                                                                                                                                                                                                                          TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: P-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                               Local
                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                          TELEPHONE:
                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122
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                                                                             Similarity
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                EASGIGPEVPDDRDFEPSLGPVCPFRCQCHLRVVQCSDLGLDKVPKDLPPDTTLLDLQNN 61
                                                                                                                                                                           amino acid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KITEIKDGDFKNLKNLHALILVNNKISKVSPGAFTPLVKLERLYLSKNQLKELPEKMPKT
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: UNITED STATES
                                                                                                                                                                                            96 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MULLEN, DANIEL G.
VENTION: DECORIN FRAGMENTS AND METHODS OF INHIBITING CELL REGULATORY FACTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIERSCHBACHER, MICHAEL D. CARDENAS, JOSE CRAIG, WILLIAM
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                                                                                                                                                                                                                                                          619-535-9001
                                                                                                                                            protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41.7%;
                                                                             28.5%; Score 488; DB 1; 100.0%; Pred. No. 4.3e-40;
                                                                                                                                                                                                                                                                                                                                                                          US 07/865,652
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                                                                                                                                                                                                                                                                                          P-LA 1454
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                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Version #1.25
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                                                                                           Length 96
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63
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APPLICANT: Watson, James D.

APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
FITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
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                                                                                                                                                                                           APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James G
APPLICANT: Kumble, Krishana
CURRENT APPLICATION NUMBER: US/09/312,283
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 425
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 305
LENGTH: 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PastSEQ for Windows Version 3.0 SEQ ID NO 305.
                                                                                                                                                                                                                                                                                                                                  GENERAL
                                                                                                                                                                                                                                                                                                                                                    Sequence 305, Application US/09312283C Patent No. 6573095
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Best Local
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                                                                                                                                APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated from Skin
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 11000.1011c2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 649
TYPB: PRT
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                                                                                                                                                                                                                                                                                                                                INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 NNKISKVSPGAFTPLVKLERLYLSKNOLKELPEKMPKTLOELRAHENEITKVRKVTFNGL 143
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89
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                                                                                                                                                                                                               Strachan, Lorna
Sleeman, Matthew
Onrust, Rene
Murison, James G.
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                                                                                                            US/09/312,283C
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Pred. No. 1.6e-24;
9; Mismatches 86
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TOPOLOGY: linear

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US-08-303-238-1
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                                                                           CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: KONSKI, ANTOINETTE F.
REGISTRATION NUMBER: 94,202
REFERENCE/DOCKET NUMBER: P-LA
TELECOMMUNICATION INFORMATION:
                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                            ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
SEQUENCE CHARACTERISTICS:
LENGTH: 376 amino acid
                                                                                                                                                                                                                                                                                                                                                                                     STREET: 45.
STREET: 45.
CITY: SAN DIEGO
CTATE: CALIFORNIA
TOUTED ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                TELEPHONE:
                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                144 NOMIVIE---LGTNPLKSSGIENGAFQGMKKLSYIRIADTNITSIPQGLPPSLTELHLDG 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201 NKISRVDAASLKGLNNLAKLGLSFN------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------ELKVORIYLYHNSLDEFPTNLPKYVKELHLQENNI---RTITYDSL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                      E: CAMPBELL AND FLORES
4370 LA JOLLA VILLAGE DRIVE, SUITE 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RUOSLAHTI, ERKKI I.
LONGAKER, MICHAEL T.
WHITBY, DAVID J.
HARPER, JOHN R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIERSCHBACHER, MICHAEL D.
BORDER, WAYNE A.
                                                 619-535-8949
                                                                                                                                                                                                                                                                                                                                                                                       UNITED STATES
                                                                619-535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INHIBITORS OF CELL REGULATORY FACTORS AND METHODS FOR PREVENTING OR REDUCING
                                                                                                                                                                                  US 07/978,931
                                                                                                                                                                                                                                                   US/08/303,238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49; Mismatches
                                                                                                  P-LA 9453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 341; DB 4;
Pred. No. 1.6e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86; Indels
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US-08-458-834-1
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US-08-303-238-1
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Best Local Similarity
                                        FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION UNDATA:
APPLICATION UNMBER: US 07/978,931
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: KONSKI, ANTOINETTE F.
REGISTRATION UNMBER: 34,202
REFERENCE/DOCKET NUMBER: P-LA 9453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: RUOSLA
APPLICANT: LONGAK
                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: FROP COMPATIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
TELECOMMUNICATION INFORMATION: TELEPHONE: 619-535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: PIERSCHBACHER, MICHAEL D.
APPLICANT: BORDER, WAYNE A.
TITLE OF INVENTION: INHIBITORS OF CELL REGULATORY FACTORS
TITLE OF INVENTION: AND METHODS FOR PREVENTING OR REDUCING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: SAN DIEGO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179 RELHLDHNQISRVPNNALEGLENLTALYLQHDEIQEVG---SSMRGLRSLILLDLSYNHL 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 SIQEGVFDNATGLLWIALHGNQITSDKVGRKVFSKLRHLERLYLDHNNLTRMPGPLPRSL 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             CALIFORNIA: UNITED STATES
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4370 LA JOLLA VILLAGE DRIVE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WHITBY, DAVID J.
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LONGAKER, MICHAEL T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RUOSLAHTI,
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                                                9453
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GENERAL INFORMATION:
APPLICANT: Goodman, Corey
APPLICANT: Kid, Thomas
APPLICANT: Hose, Katja
APPLICANT: Brose, Katja
APPLICANT: Tessier-Lavigne, Marc
ITITE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REFERENCE: B98-031-3
CURRENT APPLICATION NUMBER: US/09/191,647
CURRENT FILING DATE: 1998-11-13
EARLIER FILING DATE: 1997-11-14
EARLIER FILING DATE: 1997-11-14
EARLIER FILING DATE: 1997-11-14
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US-09-191-647-7
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EARLIER FILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
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Best Local :
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LENGTH: 376 amino acids
                                                                                                                                                                                                                                                                                    ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                               LENGTH: 1480
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TOPOLOGY: linear
                                                                                                                                                                                                 Local
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333 FITELPPKSFSSFRRLRRIDLSNNNISRIAHDALSGLKQLTTLVLYGNKIKDLPSGVFKG
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                                       62 KITEIKOGDFKNLKNIHALILVNNKISKVSPGAFTPLVKLERLYLSKNQLKELPEKMPKT 121
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                                                                                                                            2 EASGIGPEVPDDRDFEPSLGPVCPFRCQCHLRVVQCSDLGLDKVPKDLPPDTTLLDLQNN 61
                                                                                                                                                                                                 Similarity
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                                                                                     KCSGLTEHAPMECGAENS----CPHPCRCADGIVDCREKSLTSVPVTLPDDTTDVRLEQN
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                                                                                                                                                                            Conservative
                                                                                                                                                                                              18.9%; Score 323; DB 3; Length 1480; 25.3%; Pred. No. 3.2e-22;
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                                                                                                                                                                          61; Mismatches 129;
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                                                                                                                                                                          Indels 102;
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; ORGANISM: Drosophila melanogaster
US-09-540-245A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/09540245A Patent No. 6270984 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 18.9%; Score 323; DB 3; Length 1480; Best Local Similarity 25.3%; Pred. No. 3.2e-22; Matches 99; Conservative 61; Mismatches 129; Indels 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Tessier-Lavigne, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REFERENCE: B98-031-3
CURRENT APPLICATION NUMBER: US/09/540,245A
CURRENT FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 60/065,544
PRIOR PILING DATE: 1997-11-14
PRIOR APPLICATION NUMBER: 60/081,057
PRIOR APPLICATION NUMBER: 60/081,057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 19
NUMBER OF SEQ ID NOS:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1480
                                                                                                                                                                                                                                          393
215 NNLAKLGLSFNSISAVDNGSLANTPHLRELHLDNNKLTRVPGG--LAEHKYIQVVYLHNN : | | : | | | | | | : : : | ::|
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                                                                   511 GECRMDSDCPAMCHCEGTTVDCTGRRLKEIPRDIPLHTTELLLUDNELGRISSDGLFGRL
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                                                                                                                                                                                                                                                                                                                                                                                                                 277 KCSGLTEHAPMECGAENS----CPHPCRCADGIVDCREKSLTSVPVTLPDDTTDVRLEQN
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Brose, Katja
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                                                                                                            -ITSIPQGLPPSLTELHLDGNKISRVDAASLKG-L
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APPLICANT: APPLICANT:

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RESULT 25
PCT-US91-09055-2
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SEQ ID NO 7
LENGTH: 1480
           Sequence 2, Application PC/TUS9109055
GENERAL INFORMATION:
APPLICANT: Rothberg, Jonathan Marc and Artavanis-Tsakonas,
TITLE OF INVENTION: Purified SLIT protein and Sequence Elen
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REFERENCE: B98-031-3
CURRENT APPLICATION NUMBER: US/09/540,153
CURRENT FILING DATE: 2000-03-31
FRIOR APPLICATION NUMBER: 09/191,647
PRIOR FILING DATE: 1998-11-13
FRIOR PRIOR PRIOR THING DATE: 1998-01-07
NUMBER: 07 SEQ ID NOS: 14
NUMBER: 07 SEQ ID NOS: 14
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Pred. No. 3.2e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                  ----ITSIPQGLPPSLTELHLDGNKISRVDAASLKG-L 214
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                                                Elements Thereof
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TELEX: 236268
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/624,135
FILING DATE: 7-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Batth, Richard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Microsoft Word 4.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: protein-pro
NAME/KEY: 7th EGF-like repeat
LOCATION: 1353 to 1393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: developmentally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDENTIFICATION METHOD: similarity to epidermal growth OTHER INFORMATION: Involvement in receptor-ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (212) 370-1622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PFILING DATE: 19911127
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 28, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macinto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 246 Church
STREET: Suite 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Yale University
ADDRESSEE: Office of Cooperative
STREET: 246 Church Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION:
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                                          333 FITELPPKSFSSFRRLRRIDLSNNNISRIAHDALSGLKQLTTLVLYGNKIKDLPSGVFKG
                                                                                                                           277 KCSGLTEHAPMECGAENS----CPHPCRCADGIVDCREKSLTSVPVTLPDDTTDVRLEQN
122 LQELR---AHENEITKVRKVTFNGLNQMIVIELGTNPLKSSGIENGAFQGMKKLSYIRIA 178
                                                                                 62 KITEIKDGDFKNLKNLHALILVNNKISKVSPGAFTPLVKLERLYLSKNQLKELPEKMPKT
                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                             18.9%; Score 323; Conservative 61; Mismatch
                                                                                                                                                                                                                                                                                                                                              1405 to 1480
                                                                                                                                                                                                                                                                                                                                                               COOH-terminal region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Four Flank-LRR-Flank domains 37 to 910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             signal sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                  1394 to 1404
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Alternative splice segment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein-protein
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                                                                                                                                                                                                                                                                                                                                                                                                          experimental
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                                                                                                                                                                                                                                                       Length 1480;
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Query Match

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TYPE: PRT

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US-09-182-024A-5
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/063,946
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/096,420
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 640100-271
CURRENT APPLICATION NUMBER: US/09/182,024A
CURRENT FILING DATE: 1998-10-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Connolly, Time APPLICANT: Rajput, Bhanu TITLE OF INVENTION: Humar TITLE OF INVENTION: Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1480
TYPE: PRT
ORGANISM: Drosophila melanogaster
        273
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                                                                                                                        GECRMDSDCPAMCHCEGTTVDCTGRRLKEIPRDIPLHTTELLLNDNELGRISSDGLFGRL
                                                                                                                                                                                                                                                                                                                                                               FITELPPKSFSSFRRLRRIDLSNNNISRIAHDALSGLKQLTTLVLYGNKIKDLPSGVFKG 392
                                                                                                                                                                                                                                                                                                                                                                                        KITEIKDGDFKNLKNLHALILVNNKISKVSPGAFTPLVKLERLYLSKNQLKELPEKMPKT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EASGIGPEVPDDRDFEPSLGPVCPFRCQCHLRVVQCSDLGLDKVPKDLPPDTTLLDLQNN 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSLRLLLLNANEISCIRKDAFRDLHSLSLLSLYDNNIQS--LANGTFDAMKSMKTVHLA
                                           PHLVKLELKRNQLTGIEPNAFEGASHIQELQLGENKIKEISNKMFLGLHQ-LKTLNLYDN
                                                                                                                                                                                                                                                                                                                       LQELR----AHENEITKVRKVTFNGLNQMIVIELGTNPLKSSGIENGAFQGMKKLSYIRIA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QISCV-----MPGSFEHLNSLTSLNLASNP 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NISVVGSSDFCPPGHNTKKASYSGVSLFSNP 303
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      NISVVGSSDFCPPGHNTKKASYSGVSLFSNP 303
                                                                              NNLAKLGLSFNSISAVDNGSLANTPHLRELHLDNNKLTRVPGG--LAEHKYIQVVYLHNN
                                                                                                                                                                                                     KNPFICDCNLRWLADYLHKNPIETSGARCESPKRMHRRRIESLREEKFKCSWGELRMKLS
                                                                                                                                                                                                                                                                                  LGSLRLLLINANEISCIRKDAFRDLHSLSLLSLYDNNIQS--LANGTFDAMKSMKTVHLA 450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 321; DB 4; Length 1480;
Pred. No. 4.9e-22;
51; Mismatches 129; Indels 10
                                                                                                                                                                                                                                            181
                                                                                                                                                           -ITSIPQGLPPSLTELHLDGNKISRVDAASLKG-L
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US-09-182-024A-2
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US-09-312-283C-396
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                                                                                                                                         Sequence 2, Application US/09182024A Patent No. 6342370 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 18.7%; Score 321; DB 4; Best Local Similarity 25.4%; Pred. No. 5.2e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 105; Conservative
APPLICANT: Connolly, Timothy
APPLICANT: Rajput, Bhanu
TITLE OF INVENTION: Human Slit Polypeptide
TITLE OF INVENTION: Same
FILE REFERENCE: 640100-271
CURRENT APPLICATION UNMBER: US/09/182,024A
CURRENT FILING DATE: 1998-10-29
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TYPE: PRT
ORGANISM: Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 425
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Kunble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated from
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 11000.1011c2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174
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                                                                                                                                                                                                                                                                                                                                                                                                    SFNSISAVDNGSLANTPHLRELHLDNNKLTRVP----GGLAEHKYIQVVYLHNNNISVVG
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Sleeman, Matthew
Onrust, Rene
                                                                                                                                                                                                                                                                                                                         SSDFCPPGHNTKKASYSGVSLFSNPV-----
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                                                                                                                                                                                                                                                                                  --PEGAFGDISALSHLAIGANPLYCDCNMQWLSDWVKSEYKE--PGIARC 886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---YIRIADTNITSIPQGLPPSLTELHLDGNKISRVDAASLKGLNNLAKLGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------HENEITKVRKVTFNGLNOMIVIELGTNP 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60; Mismatches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -LKSSGIENGAFQ-----GMKKLS 173
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                                                                                 Polynucleotides Encoding
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; Sequence 2, Application US/09191647
    Patent No. 6046015
; GENERAL INFORMATION:
    APPLICANT: Goodman, Corey
    APPLICANT: Kid, Thomas
    APPLICANT: Brose, Katja
    APPLICANT: Brose, Katja
    APPLICANT: Mroseier-Lavigne, Marc
    TITLE OF INVENTION: Modulating Robo: Ligand In
    FILE REFERENCE: B98-031-3
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US-09-191-647-2
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; ORGANISM: Homo sapiens
US-09-182-024A-2
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SEQ ID NO 2
LENGTH: 1523
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Query Match 18.5%;
Best Local Similarity 25.7%;
Matches 101; Conservative 6
                                                                                                                             SOFTWARE: PatentIn Ver.
SEQ ID NO 2
LENGTH: 1525
                                                                            TYPE: PRT
ORGANISM: human
-09-191-647-2
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PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/096,420
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver: 2.1
                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/191,647
CURRENT FILLING DATE: 1998-11-13
EARLIER APPLICATION NUMBER: 60/065,544
EARLIER FILING DATE: 1997-11-14
EARLIER APPLICATION NUMBER: 60/081,057
EARLIER FILLING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            854 LGTNPL 859
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96;
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 60;
 Score 317; DB 3; Length 1525;
Pred. No. 1.3e-21;
60; Mismatches 120; Indels 11
                                                                                                                                                                                                                                                                                                                                     Interactions
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 Gaps
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APPLICANT: Tessier-Lavigne, Marc
ITITLE OF INVENTION: Modulating Robo: Ligand Int
FILE REFERENCE: B98-031-3
CURRENT APPLICATION NUMBER: US/09/540,245A
CURRENT FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 60/065,544
PRIOR APPLICATION NUMBER: 60/065,544
PRIOR APPLICATION NUMBER: 60/081,057
PRIOR APPLICATION NUMBER: 60/081,057
PRIOR APPLICATION NUMBER: 60/081,057
PRIOR FILING DATE: 1998-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-540-245A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Pat
SEQ ID NO 2
LENGTH: 1525
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Best Local (
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ORGANISM: human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 502 CPEKCRCEGTTVDCSNQKLNKIPEHIPQYTABLRLNNNEFTVLEATGIFKKLPQLRKINF 561
                      156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               243 ELHLDNNKLTRVP----GGLAEHKYIQVVYLHNNNISVVGSSDFCPPGHNTKKASYSGVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 TSIPQGLPPSLTELHLDGNKISRVDAASLKGLNNLAKLGLSFNSISAVDNGSLANTPHLR
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Kid, Thomas
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18.5%;
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Pred. No. 1.3e-21;
0; Mismatches 120
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-GMKKLS---
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                  -YIRIADTNI 182
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Search Job ti	дb	Ş	DЬ	Ş.	DЬ	Ş	뮹
Search completed: February 9, 2004, 11:39:48 Job time : 32 secs	b 852 IGANPLYCDCNMQWLSDWVKSEYKEPGIARC 882	299	801 TLILSYNRLRCIPPRTFDGLKSLRLLSLHGNDISVVPEGAFNDLSALSHLA 851	. 243	b 742 KVLPKGIPRDVTELYLDGNQFTLV-PKELSNYKHLTLIDLSNNRISTLSNQSFSNMTQLL 800		682 TGNPRCQKPYFLKEIPIQDVAIQDFTCDDGNDDNSCSPLSRCPTECTCLDTVVRCSNKGL 741
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 9, 2004, 09:24:09; Search time 24 Seconds (without alignments) 644.658 Million cell updates/sec

Title: Perfect score:

US-10-004-176-6 1713 1 VEASGIGPEVPDDRDFEPSL.....QPSTFRCVYVRSAIQLGNYK 329

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result

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Q9z2h4	P13605	Q9de66	042235	062702	Q9bxb1	Q06828	060938	P24014	Q9nzul	Q9nzu0	P51886
Q9z2h4 rattus norv	bos taurus	coturnix co	gallus gall	bos taurus	homo sapien	homo sapien	homo sapien	drosophila	homo sapien	homo sapien	rattus norv

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UN Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

12 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

13 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

14 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

15 Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

16 Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

17 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

18 Matting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

19 Matting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

19 Matting M., Madan J.W., Green E.D., Dickson M.C.,

10 Matting M., Schelman J.W., Green E.D., Dickson M.C.,

10 Matterfield Y.S.M., Krzywinski M.I., Skalbka U., Smailus D.E.,

10 Matterfield Y.S.M., Krzywinski M.I., Skalbka U., Smailus D.E.,

11 "Generation and initial analysis of more than 15,000 full-length

12 Muman and mouse cDNA sequences.";

12 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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MEDLINE=90073579; PubMed=2590169;
Roughley P.J., White R.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=P07585-5; Sequence=VSP 006175, VSP 006176;
PTM: The attached glycosaminoglycan chain can be either chondroitin sulfate or dermatan sulfate depending upon of origin.
SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
L; M14219; AAB00774.1; -. SE
L; L01121; AAA52301.1; JOINED
L; L01126; AAA52301.1; JOINED
L; L01127; AAA52301.1; JOINED
L; L01127; AAA52301.1; JOINED
L; L01129; AAA52301.1; JOINED
L; L01130; AAA52301.1; JOINED
L; L01130; AAA52301.1; JOINED
L; AF138300; AAA54713.1; -.
L; AF138302; AAD44714.1; -.
L; AF138302; AAP61438.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCLELULAR LOCATION: Secreted; extracellular matrix. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FAMILY. CLASS I SUBFAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Id=P07585-3;
                                                                                                             AAB00774.1; ALT SEQ.
AAA52301.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence=VSP_006173
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conectin from the miner;
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EMBL; AF491944
EMBL; BC005322
PIR; A45016; N
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CONFLICT
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GO; GO:0007397; P:histogenesis
TPR001611; LRR.
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Pfam; PF01462; LRRUT; 1.
SMART; SM00369; LRR TYP; 1.
SMART; SM00013; LRRUT; 1.
Glycoprotein; Extracellular
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AF491944; AAL92176.
BC005322; AAH05322.
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                                                                                      32
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ITSIPQGLPPSLTELHLDGNKISRVDAASLKGLNNLAKLGLSFNSISAVDNGSLANTPHL
                          LQELRAHENE I TKVRKVTFNGLNQMI VI ELGTNPLKSSGI ENGAFQGMKKLSYI RI ADTN
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                                                            KITEIKDGDFKNLKNLHALILVNNKISKVSPGAFTPLVKLERLYLSKNQLKELPEKMPKT
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                                                                                                  EASGIGPEVPDDRDFEPSLGPVCPFRCQCHLRVVQCSDLGLDKVPXDLPPDTTLLDLQNN
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ilarity 100.0%;
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/FTId=VSP 006174.
LDKV -> CLPS (in isof
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                                                                                                                                   Score 1709; DB 1;
Pred. No. 8.5e-11;
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                                                                                                                                                                                      /FTId=VAR 014351.
E -> Q (IN dbSNP:1803344).
/FTId=VAR_011975.
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FF511E871A1A52DD
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Submitted
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15-JUL-1998
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PGS2_C
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Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases
-!- FUNCTION: May affect the rate of fibrils formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Canis familiaris (Dog).
Canis familiaris (Dog).
                                                                                                                                                                                                                                                          Pfam;
Pfam;
                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 244-259 FROM N.A.
                                                                                                                                                                                                                                 SMART;
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                                                                                                                                            Leucine-r:
SIGNAL
                                                                                                                                                                                        Glycoprotein;
                                                                                                                                                                                                               SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
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28-FEB-2003
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of origin (By similarity).
SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH
SIMILARITY: CLASS I SUBFAMILY.
rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity).
SUBUNIT: Binds to type I and type II collagen, to fibronectin TGF-beta. Forms a ternary complex with MFAP2 and ELN (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity).
SUBCELLULAR LOCATION:
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PF01462; LRRNT; 1.
; SM00369; LRR TYP; 1.
; SM00013; LRRNT; 1.
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IPR000372; LRR_Nterm.
IPR003591; LRR_typ.
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ne proteoglycan II) (PG-S2)
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                                                                                                                Richardson D.W., Dodge G.R.;
"Effects of interleukin-1 beta and
expression of matrix related genes
chondrocytes.";
Submitted (DEC-1997) to the EMBL/Ge
                                                                                                                                                                                                                                                                 Equus caballus (Horse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Butheria; Perissodactyla; Equidae; Equus.
NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                Decorin precursor proteoglycan II) (DCN.
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15-JUL-1999 (Rel.
28-FEB-2003 (Rel.
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         :- FUNCTION: May affect t similarity).
- SUBUNIT: Binds to type TGF-beta. Forms a terns similarity.
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    41, Last annotation upon
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    (DS-PGII)

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LRR-T 3.

LRR-T 4.

LRR-S 3.

LRR-S 5.

LRR-T 5.

LRR-T 6.

LRR-S 7.

LRR-S 7.

LRR-S 1.

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e rate of fibrils !
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Pred. No. 3.3e
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SIMILARITY: Contains 12 leucine-rich (LRR) repeats

of origin (By similarity) SIMILARITY: BELONGS TO TH chondroitin sulfate

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LEUCINE-RICH

PROTEOGLYCAN

collaboration -

LOCATION:

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SIMILARITY: BELONGS TO THE SMALL (SLRP) FAMILY. CLASS I SUBFAMILY.

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Pfam; PF01462; LRRNT; 1.
SMART; SM00013; LRRNT; 1.
Glycoprotein; Extracellular matrix;
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InterPro; IPR001611; LRR.
InterPro; IPR000372; LRR. Nterm.
InterPro; IPR003591; LRR. typ.
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TNITSIPQGLPPSLTELHLDGNKISRVDAASLKGLNNLAKLGLSFNSISAVDNGSLANTP
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BY SIMILARITY.

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SIMILARITY).

O-LINKED (GLYCOSAMINOGLYCAN) (:
SIMILARITY).

N-LINKED (GLCNAC. . .) (POTENT:
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Pred. No. 5.46
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                                                                                                                                                                                                                                                                                                                                 4e-105;
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                                                              EMBL; AF125537; AAD23578.1; -.
EMBL; AF140770; AAD33862.1; -.
InterPro; IPR001611; LRR.
InterPro; IPR000372; LRR Neerm.
InterPro; IPR003591; LRR_typ.
Pfam; PF00560; LRR; 8.
Pfam; PF00462; LRRNT; 1.
SMART; SM00359; LRR TYD; 2.
SMART; SM00013; LRRNT; 1.
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30-MAY-2000
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                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. The use by non-profit institutions as not removed modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota;
Mammalia; E
                     Glycoprotein;
Leucine-rich:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stephenson S., Schnoke M., Vesely I.,
"Alternatively spliced version of the porcine decorin ge
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases
-!- FUNCTION: May affect the rate of fibrils formation (
                                                                                                                                                                                                                                                                                                                                                                                                                   between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stephenson S., Schnoke M., Vesely I.; "Cloning of the porcine decorin gene."; Submitted (FEB-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM SHO
STRAIN-Yorkshire; TISSUE-Aorta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: Contains 12 leucine-rich (LRR) repeats.-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE FAMILY. CLASS I SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Secreted; extracellular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of origin (By similarity)
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(Rel. 39, Last sequence update)
(Rel. 41, Last annotation updat
(cursor (Bone proteoglycan II) (P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9XSD9-1; Sequence=Displayed;
                     repeat;
Extracellular matrix; Proteoglycan; Repeat; repeat; Signal; Alternative splicing.

1 16 POTENTIAL.
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| II) (PG-
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Best Local Sim
Matches 301;
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P21793;
01-MAY-1991
01-MAY-1991
28-FEB-2003
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DOMAIN
REPEAT
SEQUENCE FROM N.A.
MEDLINE=88133946; PubMed=3435485;
Day A.A., McQuillan C.I., Termine
                                                                                                                      Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Ce
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                           DCN.
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                                                                                               NCBI_TaxID=9913;
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1991 (Rel. 18, Last sequence up
2003 (Rel. 41, Last annotation
precursor (Bone proteoglycan I
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304
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                                                                                                                                               Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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LER-T 2.
LER-S 2.
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LER-T 6.
LER-T 7.
LER-T 7.
LER-T 7.
LER-T 17.
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Pred. No. 2.3e.
12; Mismatches
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  J.D.,
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II) (PG-S2).
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     M.R.;
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                                                                                                                                                  Bovoidea
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  CARBOHYD
CARBOHYD
CARBOHYD
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J. Biol. С
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Pfam;
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SMART; SM00013; LRRNT; 1
Glycoprotein; Extracellu
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PIR; S06280; 9
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IN [3]

INTERACTION WITH MFAP2 AND ELN.

INTERACTION WITH MFAP2 AND ELN.

IX MEDLINE=21683536; PubMed=11723132;

IX MEDLINE=21683536; PubMed=11723132;

IX MEDLINE=21683536; PubMed=11723132;

IX MEDLINE=21683536; PubMed=11723132;

IX Reinboth B., Hanssen E., Cleary E.G., Gibson M.A.;

IX Reinboth B., Hanssen E., Cleary E.G., Gibson M.A.;

IX Components: biglycan forms a ternary complex with tropoelastin and microfibril-associated glycospicterin 1.";

IX J. Biol. Chem. 277:3950-3957(2002).

IX J. Biol. Chem. 277:3950-3957(
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Biochem. J. 248:801-805(1987).
[2]
SEQUENCE OF 31-54.
MEDLINE-89123388; PubMed-2914936;
Choi H.U., Johnson T.L., Pal S., Tang L.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neame P.J.;
"Characterization of the dermatan sulfate DS-PGII, from bovine articular cartilage
entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                         s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                       of origin.
SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN (SIRP) FAMILY. CLASS I SUBFAMILY.
SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
                                 the Swiss Institute of Bioinformatics and the EMBL outst pean Bioinformatics Institute. There are no restrictions non-profit institutions as long as its content is in and this statement is not removed. Usage by and for com requires a license agreement (See http://www.isb-sib.ch/an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chromatography.";
Chem. 264:2876-2884(1989).
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and skin isolated by
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collaboration in no way commercial

InterPro; IPR001611; IRR.
InterPro; IPR000372; IRR Nterm.
InterPro; IPR003591; IRR typ.
Pfam; PF00560; IRR; 9.
Pfam; PF01462; LRRNT; 1. 1 Signal.
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2234
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2238
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34
34 Extracellular matrix; Proteoglycan; CAA68702.1; 2 BY SIMILARITY.
BY SIMILARITY.
O-LINKED (GLYCOSAMINOGLYCAN) (
SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENT
N-LINKED (GLCNAC. . .) (POTENT
N-LINKED (GLCNAC. . .) (POTENT DECORIN.
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LAR-T 7. POTENTIAL. (POTENTIAL)
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ID PGS2 R
AC Q28888
DT 15-JUL
DT 15-JUL
DT 15-JUL
DT 28-FEB
DE COC.
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RP SEQUEN
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Best Local :
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Q28888; Q28608;
15-JUL-1999 (Rel
15-JUL-1999 (Rel
28-FEB-2003 (Rel
                                                                                                              TISSUE-Cartilage;
Hering T.M., Kollar J.;
Hering T.M., Kollar J.;
"The primary structure of rabbit chondrocyte decorin deduced nucleotide sequence.";
Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.
-I-FUNCTION: May affect the rate of fibrils formation (By similarity).
-I-SUBUNIT: Binds to type I and type II collagen, to fibrone of the collagen of the collagen of the collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                        SEQUENCE OF 38-358 FROM N.A.
                                                                                                                                                                                                                                                                       MEDLINE=95122319; PubMed=7822148;
                                                                                                                                                                                                                                                                                                                                                   Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                       Decorin
                                                                                                                                                                                                                                                 Zhan Q., Burrows R., Cintron C.; "Cloning and in situ hybridization
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9986;
                                                                                                                                                                                                                               invest.
   similarity).

PTM: The attached glycosaminoglycan chain can be either chondroitin sulfate or dermatan sulfate depending upon the of origin (By similarity).

SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN (SLRP) FAMILY. CLASS I SUBFAMILY.

SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
                                                                                   similarity).
SUBCELLULAR LOCATION:
                                                                                                         TGF-beta. Forms a
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(Rel. 38, Last sequence update)
(Rel. 41, Last annotation update)
(Rel. 41, Dast annotation update)
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                                                                                                                                                                                                                                                                                                                          cuniculus (Rabbit).
Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
utheria; Lagomorpha; Leporidae; Oryctolagus.
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Pred. No. 1.4
                                                                                                       and type II collagen, to fibronectin y complex with MFAP2 and ELN (By
                                                                                                                                                                                                                             36:206-215(1995)
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InterPro; IPR000372; LRR Nterm.
InterPro; IPR003591; LRR_typ.
Pfam; PF00560; LRR; 8.
Pfam; PF01462; LRRNT; 1.
SMART; SM0039; LRR TYP; 1.
SMART; SM00013; LRRNT; 1.
Glycoprotein; Extracellular matrix; Proteoglycan;
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                                            FSNPVQYWEIQPSTFRCVYVRSAIQLGNYK
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FSNPVQYWEIQPSTFRCVYMRSAIQLGNYK
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CYS_RICH.

LRR-S 1.

LRR-T 1.

LRR-T 2.

LRR-T 2.

LRR-T 3.

LRR-T 4.

LRR-T 5.

LRR-T 6.

LRR-T 7.

LRR-T 7.

LRR-T 1.

LRR-T 8.

LRR-T 1.

LRR-T
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Pred. No. 1.4e-
17; Mismatches
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RESULT 7
PGS2_SHEEP
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                                DOMAIN
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28-FEB-2003
28-FEB-2003
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SMART; SM00013; LRRNT; 1.
Glycoprotein; Extracellular matrix; Proteoglycan;
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Bovidae; Caprinae;
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MEDLINE=20113292; PubMed=10644528;
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                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                  eucine-rich
                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTE (SLRP) FAMILY. CLASS I SUBFAMILY. SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                 chondroitin sulfate or de of origin (By similarity) SIMILARITY: BELONGS TO TH
                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity).
PTM: The attached glycosaminoglycan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity).
SUBCELLULAR LOCATION: Secreted;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: May affect the rate of fibrils formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity).
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IPR000372; LRR_Nterm.
IPR003591; LRR_typ.
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31
55
74
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119
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Fignal.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence up
Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proteoglycan II) (PG-
                                                                                                                                                                                                                                                                                                                                                                                                                                     dermatan sulfate depending
             POTENTIAL.
BY SINILAR
DECORIN.
CYS-RICH.
LRR-G 1.
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LRR-T 2.
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   SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PG-S2)
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RESULT 8
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Best Local S
Matches 298
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND FRALLESSE SEQUENCE FROM N.A., AND FRALLESSE STRAIN=White leghorn; TISSUE=Cornea; STRAIN=White leghorn; TISSUE=Cornea; STRAINE=92296755; PubMed=1605630; Li W., Vergnes J.-P., Cornuet P.K., Hassell J.R.; Li W., Hass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PGS2_CHICK
P28675;
01-DEC-1992
01-DEC-1992
28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-DEC-1992 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Decorin precursor (Bone proteoglycan II) (PG-S2).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CBI_TaxID=9031;
                                   SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
                                                                                                                                                                                                                                  similarity).
SUBUNIT: Binds to type I and
                                                        chondroitin sulfate or de
of origin (By similarity)
SIMILARITY: BELONGS TO TH
(SLRP) FAMILY. CLASS I SU
                                                                                                                                                                            SUBCELLULAR LOCATION: Secreted;
                                                                                                                                   similarity).
PTM: The attached glycosaminoglycan.
                                                                                                                                                                                                 similarity)
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RESULT 9
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InterPro; IPR000372; LRR. Nterm.
InterPro; IPR0003591; LRR. Typ.
Pfam; PF00560; LRR; 10.
Pfam; PF01462; LRRNT; 1.
SMART; SM00369; LRR Typ; 2.
SMART; SM00013; LRRNT; 1.
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                                                                                                                                                                                                                                                                                                                        NITSIPQGLPPSLTELHLDGNKISRVDAASLKGLNNLAKLGLSFNSISAVDNGSLANTPH
                                                                                                          SNPVQYWEIQPSAFRCIHERSAVQIGNYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TLQELRAHENEITKVRKVTFNGLNQMIVIELGTNPLKSSGIENGAFQGMKKLSYIRIADT
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                                                                                                                                                                                                                    VRVPSGLGEHKYIQVVYLHNNKIASIGINDFCPLGYNTKKATYSGVSLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82.6%; Score 1415; DB 1;
80.2%; Pred. No. 5.1e-93;
Live 28; Mismatches 37;
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CYS-RICH.

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LRR-T 6.

LRR-T 6.

LRR-T 7.

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InterPro; IPR001611; LRR.
InterPro; IPR000372; LRR_Nterm.
InterPro; IPR003591; LRR_typ.
InterPro; IPR003591; LRR_typ.
Pfam; PF00560; LRR; 10.
Pfam; PF016402; LRRNT; 1.
SMART; SM00369; LRR_TYP; 2.
SMART; SM00013; LRRNT; 1
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Q9DE68;
28-FEB-2003
28-FEB-2003
28-FEB-2003
                                                                                                                                                                        DOMAIN
REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE=Cornea, and Sclera;
MEDLINE=20556471, PubMed=11102759;
Gorpuz L.M., Dunlevy J.R., Hassell J.R.
"Molecular cloning and relative tissue
lumican in embryonic quali cornea.";
Matrix Biol. 19:699-704(2000).
   CARBOHYD
                                                                                                                                                                                                                             Glycoprotein;
Leucine-rich
                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb
                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                          EMBL; AF125250; AAG48154.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coturnix coturnix japonica (Japanese quail).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Decorin precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                of origin (By similarity).

SIMILARITY: BELONGS TO THE SMALL LEUCINE-RI
(SLRP) FAMILY. CLASS I SUBFAMILY.

SIMILARITY: Contains 12 leucine-rich (LRR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity).
SUBUNIT: Binds to type I and type II collagen, to TGF-beta. Forms a ternary complex with MFAP2 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity).
SUBCELLULAR LOCATION: Secreted;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTM: The attached glycosaminoglycan chain can be either chondroitin sulfate or dermatan sulfate depending upon the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similarity)
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                                                                                                                                                                                                                             repeat;
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, Last annotation
one proteoglycan I
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                                                     CYS-RICH.

LRR-T 1.

LRR-T 2.

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BY SIMILARITY.
BY SIMILARITY.
O-LINKED (GLYCOSAMINOGLYCAN)
SIMILARITY).
N-LINKED (GLCNAC. . .) (POTEI
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                                                                                                                                                                                                      SIMILARITY.
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in II) (PG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expression
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on of decorin
  .) (POTENTIAL).
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Best Local S
Matches 260
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P28654;
01-DEC-1992
01-DEC-1992
28-FEB-2003
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SEQUENCE
This SWI
                                                                                                MEDLINE=95050610; PubMed=7961765; Scholzen T., Solursh M., Suzuki S., Reiter R., Morgan Buchberg A.M., Siracusa L.D., Iozzo R.V.; "The murine decorin. Complete cDNA cloning, genomic or chromosomal assignment, and expression during organoge tissue differentiation."; J. Biol. Chem. 269:28270-28281(1994).

-i- FUNCTION: May affect the rate of fibrils formation.
-i- SUBUNIT: Binds to type I and type II collagen, to TGF-beta. Forms a ternary complex with MFAP2 and E
                                                                         <del>+</del> <del>+</del>
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01-DEC-1992 (Rel. 24, Last sequence update)
02-FFEB-2003 (Rel. 41, Last annotation updat
Decorin precursor (Bone proteoglycan II) (F
                                                                                                                                                                                                                  Submitted
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Naitoh Y.,
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                                                                                                                                                                                                                                                                                 Eukaryota;
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                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                     MOUSE
                                                                                                                                                                                                                                                                        Mammalia; Eutheria;
                      similarity).
SUBCELLULAR LOCATION: Secreted; extracellular matrix.
FYM: The attached glycosaminoglycan chain can be eith
chondroitin sulfate or dermatan sulfate depending upo
of origin (By similarity).
SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOG
(SLRP) FAMILY. CLASS I SUBFAMILY.
SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
SWISS-PROT entry is
een the Swiss Instit
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VIH Swiss;
(., Suzuki
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; Metazoa; Chordata; C
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, Suzuki S.;
(JUL-1990) to the EMBL/Gen
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356
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ilarity 84.1%;
Conservative 2
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ry is copyright. It is produced through Institute of Bioinformatics and the EN
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Pred. No. 3.6e
27; Mismatches
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; BE9583C6AED7DB26 CRC64;
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Sciurognathi; Muridae; Murinae; Mus
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II) (PG-S2)
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        NPVRYWEIFPNTFRCVYVRSAIQLGNYK
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InterPro; IPR001611; LRR.
InterPro; IPR000372; LRR_typ.
InterPro; IPR0003591; LRR_typ.
Pfam; PF00560; LRR; 9.
Pfam; PF01462; LRRNT; 1.
SMART; SM00013; LRR TYP; 2.
SMART; SM00013; LRRNT; 1.
Glycoprotein; Extracellular matri
Leucine-rich repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. The use by non-profit institutions as growing modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
RELHLDNNKLTRVPGGLAEHKYIQVVYLHNNNISVVGSSDFCPPGHNTKKASYSGVSLFS
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                                               LQELRVHENEITKLRKSDFNGLNNVLVIELGGNPLKNSGIENGAPQGLKSLSYIRISDTN
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SEQUENCE OF 11-35-
MEDLINE-93154359; PubMed=1495...
MEDLINE-93154359; PubMed=1495...
Asundi V.K., Dreher K.L.;
Molecular characterization of vascular smooth deduced core protein structure and regulation cdeduced core protein structure.
InterPro; IPR001611; LRR. Nterm.
InterPro; IPR000372; LRR_Nterm.
InterPro; IPR0003591; LRR_Typ.
Pfam; PF00560; LRR; 9.
Pfam; PF00560; LRR, Typ.
SMART; SM00369; LRR_TYP; 2.
SMART; SM00013; LRR_TYP; 1.
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Pfam; |
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Q01129;
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EMBL; X59859; CAA42519.1;
PIR; S29145; S29145.
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STRAIN=Sprague-Dawley; TISSUE=Uterus;
MEDLINE=89350825; PubMed=2764879;
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STRAIN-Sprague-Dawley; TISSUE-Uterus;
MEDLINE-93003331; PubMed=1390895;
Abramson S.R., Woessner J.F.;
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i PTM: The attached glycosaminoglycan chain can chondroitin sulfate or dermatan sulfate depend of origin (By similarity).

i SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH (SLRP) FAMILY. CLASS I SUBFAMILY.

i SIMILARITY: Contains 12 leucine-rich (IRR) re
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Mammalia; Eutheria;
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Biochim. Biophys. Acta
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SUBUNIT: B
TGF-beta.
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                                                                                                                                                                                                                                                                                                                            similarity).
SUBCELLULAR LOCATION: Secret
DEVELOPMENTAL STAGE: The amc
fold during pregnancy, then
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-1993 (Rel. 25, Las
-2003 (Rel. 41, Las
n precursor (Bone p
e proteoglycan-II)
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II) (DSPG).
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SACCERRICANA H

Biglycan

precursor.

Xenopus laevis (African clawed frog). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost Amphibia; Batrzeńia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus.

d frog).
Craniata; Vertebrata; Euteleostomi;

\_TaxID=8355;

PGS1 XENLA Q9IB75; Q9IB75; 28-FEB-2003 28-FEB-2003

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Created)
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sequence update)
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                        NPVRYWQIHPHTPRCVFGRSTIQLGNYK
                                                      RELHLDNNKLTRVPGGLAEHKYIQVVYLHNNNISVVGSSDFCPPGHNTKKASYSGVSLFS
                                                                       KITEIKEGAFKNIKOLHTLILVNNKISKISPEAFKPLVKLERLYLSKNHIKELPEKLPKT
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                                                RELHLDNNKLLRVPAGLAQHKYVQVVYLHNNNISEVGQHDFCLPSYQTRKTSYTAVSLYS
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3; Mismatches
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SEQUENCE FROM N.A.
GOED T., Kubota H.Y.;
GOLO T., Kubota H.Y.;
GOLO T., Kubota H.Y.;
CDNA of biglycan of Xenopus laevis.";
"CDNA of biglycan of Xenopus laevis.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: May be involved in collagen fiber assembly
-i-arity).
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InterPro; IPR000372; LRR Nterm.
InterPro; IPR003591; LRR_typ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AB037269; BAA90246.1; -.
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-!- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
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PF01462; LRRNT; 1.
', SM00013; LRRNT; 1.
'protein; Extracellular matrix; Proteoglycan;
                                  240
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NNKITETKOGDEKNILKALILUNNKISKVSPGAFTPLVKLERLYLSKNQLKELPEKMP
                                                                                                                                                                                                                                                                                                             EASGIGEEABDDRDLEBSTCE--ACELECOCHTKAAOCSDTCTDKAAKDTEBDLLTTTTDTO
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                                                                  AKLSGIPKGLPSTLNELHLDNNKIQAIEKEDLSQYASLYRLGLGHNNIRMIENGSLSFMP
                                                                                                                                                                                                          NNKITEIKKOD
                                                                                                                                                                                                                                                                           EASGVGP-IPTESIPDVGLPPMDLCPFGCQCHLRVVQCSDLGLTSIPKNLFKDTTLLDLQ
                                                                                         TNITSIPQGLPPSLTELHLDGNKISRVDAASLKGLNNLAKLGLSFNSISAVDNGSLANTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           email to license@isb-sib.ch).
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BIGLYCAN
CYS-RICH
LIRR-S 1
LIRR-T 1
LIRR-T 2
LIRR-T 3
LIRR-T 4
LIRR-T 4
LIRR-T 6
LIRR-T 6
LIRR-T 6
LIRR-T 7
LIRR-T 
                                                                                                                                                                                                                                                                                                                                                             Score 1022; DB 1;
Pred. No. 3.3e-65;
                                                                                                                                                                                                                                                                                                                                                                                                                   53ADF7E7E3BDC528 CRC64;
                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                               Length
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This SWI
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TISSUE-Vascular smooth muscle;

MEDINE-11184222; PubMed=2081545;

MEDINE-11184222; PubMed=2081545;

Dreher K.L., Asundi V.K., Matzura D., Cowan

Vascular smooth muscle biglycan represents

proteoglycan within the arterial wall.";

Bur. J. Cell Biol. 53:296-304(1990)
        CHAIN
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                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for cor entitles requires a license agreement (See http://www.isb-sib.ch/aror send an email to license@isb-sib.ch).
                                                                                                                            SIGNAL
                                                                                                                                                                                  Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1996
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P47853;
01-FEB-1996
                                                                                                                                                           SMART; SM0001
Glycoprotein;
                                                                                                                                                                                         InterPro; IPR000372; I
InterPro; IPR003591; I
Pfam; PF00560; LRR; 9.
                                                                                                                                                                                                                                     EMBL; U17834; AAA587
PIR; S32793; S32793.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
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                                                                                                                                                                                                                           InterPro; IPR001611;
                                                                                                                                                                                                                                                                                                                                                       PTM: The two attached glycosaminoglycan chains can be e chondroitin sulfate or dermatan sulfate (By similarity) SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLY (SIRP) FAMILY. CLASS I SUBFAMILY.
SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                      similarity).
TISSUE SPECIFICITY: Found in several connective
                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity).
SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity).
SUBUNIT: Forms a ternary complex with MFAP2 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: May be
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                                                                                                                                                           SM00013; LRRNT; 1. rotein; Extracellular
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FNNPVPYWEVQPATFRCVTDRLAIQFGNYR
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(Rel. 33, Last sequence update)
(Rel. 41, Last annotation update)
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Rodentia;
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CYS-RICH.
LRR-T 1.
LRR-T 1.
LRR-T 2.
LRR-S 2.
LRR-T 3.
LRR-T 4.
LRR-T 5.
LRR-T 5.
LRR-T 6.
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                                                                                                                                       POTENTIAL
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Sciurognathi; Muridae; Murinae; Rattus
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Best Local S
Matches 190
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PGS1_MOUSE

P28653; Q61355;

01-DEC-1992 (Rel. 24, C

01-DEC-1992 (Rel. 24, L

15-SEP-2003 (Rel. 42, L
                                                                                                                  [2]
SEQUENCE FROM N.A.
STRAIN=NIH Swiss; TISSUE=Embryo;
MEDLINE=94319033; PubMed=8043960;
MEDLINE=94319033; PubMed=8043960;
Rau W., Just W., Vetter U., Vogel W.;
Rau W., Just W., Tepeat in the mouse biglycan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
CARBOHYD
DISULFID
DISULFID
SEQUENCE
SEQUENCE FROM N.A.
TISSUEBreast, and Kidney;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Gr
Klausner R.D., Collins F.S., Wagne
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=NIH Swiss; TISSUE=Fibroblast;
Nairoh Y., Suzuki S.;
Submitted (JUL-1990) to the EMBL/Gen
                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
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Last annotation update
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 d E.A., Grouse
.S., Wagner L.,
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LRR-T 8.

O-LINKED (GLYCOSAMINOGLYCAN) (;
SIMILARITY).

O-LINKED (GLYCOSAMINOGLYCAN) (;
SIMILARITY).

N-LINKED (GLCNAC. . .) (POTENT
N-LINKED (GLCNAC. . .) (POTENT
BY SIMILARITY.

BY SIMILARITY.
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1; Mismatches
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Pred. No. 1.
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Hopkins,R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., RA Hopkins,R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., RA Brownstein M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., RA Romstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C., RA Romstein M.J., WcEwan P.J., Morenan K.J., Malek J.A., Gunaratne P.H., RA Rodrigues S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Parce. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the EMropean Bioinformatics Institute. There are no restrues by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-s or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                            chondroitin sulfate or dermatan sulfate or dermatan sulfate or The SMALL LEUC (SLRP) FAMILY. CLASS I SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expression and distribution in the knee jo
Biochem. J. 355:577-585(2001).
-I- FUNCTION: May be involved in collagen
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MEDLINE=21210929;
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TISSUE SPECIFICITY:
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K., Salminen H.J.,
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                             oved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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NL; 1.20276; AAA64350.1; -.

NL; BC005452; AAH05452.1; -.

NL; BC019502; AAH19502.1; -.

NL; Y11758; CAA72422.1; -.

N; S20811; S20811. PF00560; LRR; 9.
PF01462; LRRNT; 1.
; SM00013; LRRNT; 1.
protein; Extracellular 20 38 64 83 104 128 152 173 197 repeat; # Signal.

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242 LRR Nterm. LRR\_typ. matrix; Proteoglycan; BIGLYCAN.
CYS-RICH.
LRR-S 1.
LRR-T 1.
LRR-T 2.
LRR-S 2.
LRR-T 3.
LRR-T 4.
LRR-S 3. POTENTIAL Repeat;

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Best Local Similarity
Matches 190; Conserv
                                                                                                                                                            SEQUENCE FROM N.A.
Richardson D.W., Dodge G.
"Dose dependent effects o
related genes in equine a
Submitted (NOV-1997) to t
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046403; Q9N1U5;

30-MAY-2000 (Rel. 39, Last sequence upon

30-MAY-2000 (Rel. 39, Last annotation of the component of the component
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Mammalia; Eutheria; F
NCBI TaxID=9796;
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CARBOHYD
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Equus caballus (Horse).
Eguaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
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             "A comparative gene map of the horse Genome Res. 9:1239-1249(1999).
-!- FUNCTION: May be involved in coll
                                                                                                        SEQUENCE OF 150-192 FROM N.A. MEDLINE=20082971; PubMed=10613847;
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                                                                    Caetano A.R.,
Bowling A.T.,
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                                                                  Shiue Y.L., I Murray J.D.;
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sffects of corticosteroids on
equine articular chondrocytes
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Pfam; PF01462; LRRNT; 1.
SMART; SM00013; LRRNT; 1
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EMBL; AF135020; AAF64248.1; -.
InterPro; IPR001611; LRR.
InterPro; IPR000372; LRR Nterm.
InterPro; IPR003591; LRR-typ.
DFam. DF00560: LDB. 8
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Chopdroitin sulfate or dermatan sulfate (By similarity)
SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLY
(SLRP) FAMILY. CLASS I SUBFAMILY.
SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
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SUBCELLULAR LOCATION:
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                                                                NNKITEIKOGDEKNIKNIHALIILVNNKISKVSPGAFTPLVKLERLYLSKNQLKELPEKMP
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AKLTGI PKDLPETLNELHLDHNKI QAI ELEDLLRYSKLYRLGLGHNQIRMI ENGSLSFLP
                                 TNITSIPQGLPPSLTELHLDGNKISRVDAASLKGLNNLAKLGLSFNSISAVDNGSLANTP
                                                                                                                                         NNEISELRKDDFKGLQHLYALVLVNNKISKIHEKAFSPLRKLQKLYISKNHLVEIPPNLP
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SIMILARITY)
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CYS-RICH.
LRR-S 1.
LRR-T 1.
LRR-T 2.
LRR-S 2.
LRR-S 3.
LRR-T 3.
LRR-S 3.
LRR-S 3.
LRR-S 4.
LRR-T 6.
LRR-T 6.
LRR-T 6.
                                                                                                                                                                                                                                                                                   Pred. No. 1.7e-62;
3; Mismatches 86;
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Pred. No. 1.
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BY SIMILARITY.
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SIMILARITY).
N-LINKED (GLCNAC. . .) (POTE
N-LINKED (GLCNAC. . .) (POTE
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BY SIMILARITY.
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There are no restrictions
ang as its content is in
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RESULT 16
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046390;
30-MAY-2000
       CHAIN
DOMAIN
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.
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-!- PTM: The two attached glycosaminoglycan chains can be enchondroitin sulfate or dermatan sulfate (By similarity)
-!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLY.

(SLRP) FAMILY. CLASS I SUBFAMILY.
-!- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
                                                                                                                                                                                                                                                                                                                                                Pfam; PF00560; LRR; 8.
Pfam; PF01462; LRRNT; 1.
SMART; SM00013; LRRNT; 1.
Glycoprotein; Extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Choroid plexus;
Bruett L., Clements J.E.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
-i-.FUNCTION: May be involved in collagen fiber assembly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazōa; Chor
Mammalia; Eutheria; Ceta
Bovidae; Caprinae; Ovis.
NCBI_TaxID=9940;
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30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Biglycan precursor (Bone/cartilage proteoglycan
                                                                                                                                                                                                                                                                                                       SIGNAL
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SUBUNIT: Forms a ternary complex with
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SUBCELLULAR LOCATION:
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TISSUE SPECIFICITY:
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IPR000372; LRR_Nterm.
IPR003591; LRR_typ.
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Metazoa;
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                                                                                                                                                                                                                                                                                                                           Signal.
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  POTENTIAL.
BY SIMILARITY.
BIGLYCAN.
CYS-RICH.
LRR-T 1.
LRR-T 1.
LRR-T 2.
LRR-T 2.
LRR-T 3.
LRR-T 3.
LRR-T 4.
LRR-T 4.
LRR-T 5.
LRR-T 5.
LRR-T 5.
LRR-T 6.
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cora; Bovoidea;
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Query Match
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Matches 189
SEQUENCE FROM N.A.

KMEDLINE-91317791; PubMed=1860845;
Fisher L.W., Heegaard A.M., Vetter U., Vog
Termine J.D., Young M.F.;
"Human biglycan gene. Putative promoter, in
chromosomal localization.";
J. Biol. Chem. 266:14371-14377(1991).
[3]
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CARBOHYD
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DISULFID
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REPEAT
CARBOHYD
                                                                                                MEDIINE-89174714; PubMed=2647739;
Risher L.W., Termine J.D., Young M.F.;
"Deduced protein sequence of bone small proteoglycan I (biglycan) shows homology with proteoglycan II (decorin) and several nonconnective tissue proteins in a variety of species.";
J. Biol. Chem. 264:4571-4576(1989).
                                                                                                                                                                                                                                                                           P21810; P13247;
01-JAN-1990 (Rel. 13, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-SEP-2003 (Rel. 42, Last amotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                           SEQUENCE FROM TISSUE=Bone;
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                                                                                                                                                                                                                                               Homo sapiens (Human).
                                                                                                                                                                                                                                                                    Biglycan
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Primates;
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343
369
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LRR-T 7.

LRR-T 8.

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SIMILARITY).

O-LINKED (GLYCOSAMINOGLYCAN) (
SIMILARITY).

N-LINKED (GLCNAC. . .) (POTENT
N-LINKED (GLCNAC. . .) (POTENT
N-LINKED (GLCNAC. . .) (POTENT
BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.
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RX MEDLINE=2338257; PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altachul S.F., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

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Altachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Altachenko L., Molevan P.J., Molevana G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Altachenko S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunararne P.H.,

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Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

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Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

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Rahey J., Helton E., Schein J.W., Schmutz J., Myers R.M.,

Rahey J., Hellon E., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length

Thuman and mouse cDNA sequences.",

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-95187185;
Just W., Rau W., 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fisher L.W., Hawkins G.R., Tuross N., Termine J.D.; "Purification and partial characterization of small proteoglycans and II, bone sialoproteins I and II, and osteonectin from the mine compartment of developing human bone."; J. Biol. Chem. 262:9702-9708(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=90073579; PubMed=2590169;
Roughley P.J., White R.J.;
"Dermatan sulphate proteoglycans of human articular
properties of dermatan sulphate proteoglycans I and
Biochem. J. 262:823-827(1989).
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PTM: The two attached glycosaminoglycan chains can be echondroitin sulfate or dermatan sulfate (By similarity)
SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLY
(SLRP) FAMILY. CLASS I SUBPAMILY.
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SUBUNIT: Fo
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TISSUE SPECIFICITY: Found in several
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SUBCELLULAR LOCATION:
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   SWISS-PROT
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Pfam; PF01462; LRRNT; 1.
SMART; SM00013; LRRNT; 1
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(GLCNAC. . .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          structural constituent;
                                                                                                                                                                                       N REF. 1).
N REF. 1).
SCD3B3E CRC64;
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                                                                                                                                                                     Length 368;
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HEALTH PRESIDENT PROCESSION OF THE PROCESSION OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Cartilage;
TISSUE=Cartilage;
MEDLINE=89255324; PubMed=2656687;
Neame P.J., Choi H.U., Rosenberg L.C.;
"The primary structure of the core protein of the small proteoglycan (PG I) from bovine articular cartilage.";
J. Biol. Chem. 264:8653-8661(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PGS1_BOVIN S
P21809; P79259;
01-MAY-1991 (Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                       USUENCE OF 38-63.
SEQUENCE OF 38-63.
TISSUE=Cartilage;
MEDLINE=89123388; PubMed=2914936;
MEDLINE=89123388; PubMed=2914936;
                                                                                 in articular cartilages.

-!- PTM: The two attached glycosaminoglycan chains can technodroitin sulfate or dermatan sulfate.
-!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTECTION (SLRP) FAMILY. CLASS I SUBFAMILY.
-!- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
                                                                                                                                                                                                                                               MEDLINE=21683536; PubMed=11723132; Reinboth B., Hanssen E., Cleary E.G., Gibson M.A.; "Molecular interactions of biglycan and decorin wi components: biglycan forms a ternary complex with microfibril-associated glycoprotein 1."; J. Biol. Chem. 277.3950.3957(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96113563; PubMed=8673009;
Xu J.H., Radhakrishnamurthy B., Srinivasan &
"Primary structure of bovine aorta biglycan
cloned CDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BOVIN
        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                 "Characterization of the dermatan sulfate DS-PGII, from bovine articular cartilage a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus (Bovine).
Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Ce
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1991 (Rel. 18,
15-JUL-1998 (Rel. 36,
15-FEB-2003 (Rel. 41,
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                                                                                                                                                                                                                                                                                                                                                                                     Chem.
                                                                                                                                                                                                                                                                                                                                                                                  chromatography.";
Chem. 264:2876-2884(1989).
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and skin isolated by
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SIGNAL
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      STANDARD;
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modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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InterPro; IPR003591;
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                                       KTLQELRAHENEITKVRKVTENGLNQMIVIELGTNPLKSSGIENGAFQGMKKLSYIRIAD
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57.0%;
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LRR_Nterm.
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N-LINKED
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Pred. No. 6.3
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(GLYCOSAMINOGLYCAN).
(GLCNAC. . .).
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Query Match
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Matches 189
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InterPro; IPR000372; LRR. Nterm.
InterPro; IPR003591; LRR. typ.
Pfam; PF00560; LRR, 8.
Pfam; PF01462; LRRNT; 1.
SMART; SM00013; LRRNT; 1.
Glycoprotein; Extracellular matr;
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15-JUL-1998 (Rel. :
15-JUL-1998 (Rel. :
28-FEB-2003 (Rel. :
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Bukaryota; Metazoa; Chordata; (
Mammalia; Eutheria; Carnivora;
                                                                  CARBOHYD
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                                                                                                                                                                                                                                           REPEAT
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PTM: The two attached glycosaminoglycan chains can be eithe chondroitin sulfate or dermatan sulfate (By similarity).

SIMILARITY: BELONGS TO THE SWALL LEUCINE-RICH PROTEOGLYCAN (SLRP) FAMILY. CLASS I SUBFAMILY.

SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity).
SUBUNIT: Forms a ternary
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SUBCELLULAR LOCATION:
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ION: May be
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36, Last sequence update)
41, Last annotation update)
r (Bone/cartilage proteoglycan
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                56.8%;
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BY SIMILARITY.

BIGLYCAN.

CYS-RICH.

LRR-T 1.

LRR-T 1.

LRR-T 3.

LRR-T 3.

LRR-T 4.

LRR-T 5.

LRR-T 7.

LRR-T 6.

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LRR-T 1.

LRR-T 
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                Score 972.5;
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; Fissipedia; Canidae;
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                .e-61;
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Canis.
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Q9BXNI; Q96K79; Q96LD0;
28-FEB-2003 (Rel. 41, Case
28-FEB-2003 (Rel. 41, Last
28-FEB-2003 (Rel. 41, Last
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MEDLINE=21192276; PubMed=11152692;
MEDLINE=21192276; PubMed=11152692;
                                    TISSUE-Embryo;
Isogai T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Sugawara I Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara I Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi Watanabe S., Ximura K., Murakawa K., Ishida S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Ninoniya K., Iwayanagi T.;
"NEDO human CDNA sequencing project.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                    MEDILINE=21472263; PubMed=11587855; Zawa Y., Yokokoji Yamada S., Murakami S., Matoba R., Ozawa Y., Yokokoji Ikezawa K., Takayama S.-I., Matsubara K., Okada H.; "Expression profile of active genes in human periodont isolation of PLAP-1, a novel SLRP family gene."; Gene 275:279-286(2001).
                                                                                                                                                                                                                                                                                              "Identification and leucine-rich repeat biglycan.";
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Eukaryota; Metazoa;
Mammalia; Eutheria;
 PARTIAL SEQUENCE F
MEDLINE=21192277;
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precursor (Periodontal ligament associated
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 FROM N.A. ; PubMed=11152695;
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Pfam; PF01462; LRRNT; 1.
SMART; SM00013; LRRNT; 1.
Glycoprotein; Extracellular matrix; Signal; Repeat;
Glycoprotein; Extracellular matrix; Signal; Repeat;
Glycoprotein; Extracellular matrix; Signal; Repeat;
Glycoprotein; Polymorphism; Triplet repeat e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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EMBL; AY029191; AAX31800.1; -.
EMBL; AX027359; BAB55060.1; -.
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FKNLKNLHALI LVNNKI SKVSPGAFTPLVKLERLY LSKNQLKELPEKMPKTLQELRAHEN
                                     PRSHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKEND
                                                                 PDDRDFEPSLGPVCPFRCQCHLRVVQCSDLGLDKVPKDLPPDTTLLDLQNNKITEIKDGD
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B., Hoeoek M., Mayne R.;
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       RP SEQUENCE FROM N.A.

CSTRAIN=CS7BL/6J; FISSUE=Skin;

RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Pukuda S.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Kasukawa T., Salto R.,

RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Alzawa K., Nishi K., Kiyosawa H., Kasukawa T., Salto R.,

RA Alzawa K., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Salto R.,

RA Salto T., Okazaki Y., Gojobori T., Batalov S., Casavant T.,

RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

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RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G.,

RA Schriml L.M., Stabli F., Suzuki R., Toylita N., Bandao M.F.,

RA Blake J., Boffelli D., Hofmann M., Carninoi P., de Bonaldo M.F.,

RA Blake J., Bult C., Fletcher C., Fujita M., Gariboddi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Hyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Mordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seriota Y., Storch K.-F.,

RA Suzuki H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L.,

Wanshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                  Henry S.P., Takanosu M., Boyd T.C., Mayne P.M., Ebers Zhou W., de Crombrugghe B., Hoeoek M., Mayne R., "Expression pattern and gene characterization of aspodiscovered member of the leucine-rich repeat protein J. Biol. Chem. 276:12212-12221(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=C57BL/6 X 129/SvJ; TISSUE=Aorta;
MEDLINE=21192276; PubMed=11152692;
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Mammalia; Eutheria;
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(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
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'ion of asporin famil
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"Functional annota...
Nature 409:685-690(2001).

-!- SUBCELLULAR LOCATION: Secreted; extrac-
-!- similarity).

-!- TISSUB SPECIFICITY: Higher expression in heart, alf
-!- TISSUB SPECIFICITY: Higher expression in heart in the second in the s
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           SIGNAL
PROPED
CHAIN
DOMAIN
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restriction use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for centities requires a license agreement (See http://www.isb-sib.ch/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01462; LRRNT; 1.
SMART; SM00013; LRRNT; 1
Glycoprotein; Extracellu
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InterPro; IPR001611; LRR.
InterPro; IPR000372; LRR_Nterm.
InterPro; IPR0003591; LRR_typ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SLRP) FAMILY. CLASS I SUBFAMILY. SIMILARITY: Contains 12 leucine-rich CAUTION: Ref.3 sequence differs from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mandible (alveolar bone) and a strong expression is observed in sagittal sections of the subcutaneous muscles or panniculus carnosus of the thorax, trunk, and head/ neck (platysma muscle) region. Very little expression is detected in the major parenchymal organs (with the exception of the large bronchi of the lung). Its expression is prominent in the developing mouse skeleton, particularly in the perichondrium/periosteum of cartilage/bone, and is also found in other specialized connective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH (SLRP) FAMILY. CLASS I SUBFAMILY.
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tissues such as tendon, sclera, the connective tissue sheath
surrounding muscle and dermis. In the sclera of the eye it is
first detected at 15.5 dpc and stronger expression was detected
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685-690(2001).
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POTENTIAL.
POTENTIAL.
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CYS-RICH.
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LRR-T 2.
LRR-T 2.
LRR-T 3.
LRR-T 3.
LRR-T 3.
LRR-T 5.
LRR-S 3.
LRR-T 5.
LRR-T 5.
LRR-T 6.
LRR-S 4.
LRR-S 7.
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Matches 173;
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                                                                                                       "Cloning and sequencing Submitted (JUN-1999) to -i- FUNCTION: May be inv
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                                                                                                                                                                                                                                                                                          Biglycan
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                                                                                                                                                  TISSUE=Skin;
                                                                                                                                                          SEQUENCE OF 138-272 FROM N.A.
                                                                                                                                                                               Submitted
                                                                                                                                                                                        anao
                                                                                                                                                                                                FISSUE=Aorta;
                                                                                                                                                                                                            SEQUENCE OF 1-137
                                                                                                                                                                                                                            NCBI_TaxID=9823;
                                                                                                                                                                                                                                         Bukaryota;
Mammalia;
                                                                                                                                                                                                                                                            Sus scrofa
                                                                                                                                                                                                                                                                               Biglycan precursor (Fragments).
                                     similarity).
TISSUE SPECIFICITY:
in articular cartile
                                                                                      similarity).
SUBUNIT: Forms a
         chondroitin sulfate or SIMILARITY: BELONGS TO
                             in a
                                                                   similarity).
SUBCELLULAR LOCATION:
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                            rticular cartilages.
The two attached glycosaminoglycan chains can be either
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                                                                                       ternary complex with MFAP2 and
                                                                                                           involved
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                                                                                                                  Reno C.R., Olson M.E., Hart D.A.; of porcine matrix molecules."; the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                              the EMBL/GenBank/DDBJ databases.
                                                Found
                                                                    Secreted;
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THE SMALL SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62;
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POLY-ASP.
BY SIMILARITY.
O-LINKED (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 925.5;
Pred. No. 2.2e
62; Mismatches
                                                                                                        in collagen
                                                in several
                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A50C4C82AABCFC35 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                            370
                                                                                                                                                                                                                                                                                                                                                                                                             327
                                                                                                                                                                                                                                                                                        proteoglycan
                                                                    extracellular
           LEUCINE-RICH
                                                                                                                                                                                                                                                                                                                                           272
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                                               connective
                                                                                                           fiber assembly
                   (By
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                                                                   matrix
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Sus.
                                               tissues, specially
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Best Local (
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                                                                                                                                                                                                                                                                                                                      REPEAT
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REPEAT
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CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF054419; AAG39274.1; -. EMBL; AF159382; AAF19153.1; -.
                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein; Extracellular matrix;
                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: Contains at least 9 leucine-rich (LRR) repeats.
                                  270
                                                300
                                                                 210
                                                                                                                180
                                                                                                                                                                                                                                                                                                                                                                                                                                    .ne-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF01462; LRRNT; 1.
; SM00013; LRRNT; 1.
                                                                                                                                                                                                                              129;
                                                                                                                                                                              60
                                                                                                                                                                                              40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF00560; LRR; 4.
                                                                                                                                                                                                                                      Similarity
                                                  FSN
                                                                                                            TNITSIPQGLPPSLTELHLDGNKISRVDAASLKGLNNLAKLGLSFNSISAVDNGSLANTP
                                                                 TLRELHLDNNKLSRVPAGLPDLKLLQVVYLHTNNITKVGVNDFCPVGFGVKRAYYNGISL
                                                                             HLRELHLDNNKLTRYPGGLAEHKYIQVYYLHNNNISVYGSSDFCPPGHNTKKASYSGVSL
                                                                                              AKLTGI PKOLPETLNELHLDHNKI QAI ELEDLLRYSKLYRLGLGHNQIRMI ENGSLSFLP
                                                                                                                                            KTLQELRAHENEITKVRKVTFNGLNQMIVIELGTNPLKSSGIENGAFQGMKKLSYIRIAD
                                                                                                                                                              NNDISELRKDDFKGLQHLYALVLVNNKISRSTRRPSAP-
                                                                                                                                                                             NNKITEIKDGDFKNLKNLHALILVNNKISKVSPGAFTPLVKLERLYLSKNOLKELPEKMP 119
                                                                                                                                                                                             EASGADSTSGIPDLDALPPTFSAMCPFGCHCHLRVVQCSDLGLKAVPKEISPDTTLLDLQ
                                                                                                                                                                                                             EASGIGPE---VPDDRDFEPSLGPVCPFRCQCHLRVVQCSDLGLDKVPKDLPPDTTLLDLQ
                                                                                                                                                                                                                                                               272 AA;
                                                                                                                                                                                                                                                                      64
272
                                                                                                                                                                                                                              Conservative
                                  272
                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat;
                                                                                                                                                                                                                                                                                             48
                                                                                                                                                                                                                                                                                                                                                                                      ; Signal.
19
37
272
77
103
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                                                                                                                                                                                                                                                                                                             42
                                                                                                                                                                                                                                                               30457
                                                                                                                                                                                                                                                              WW;
                                                                                                                                                                                                                              38;
                                                                                                                                                                                                                          Pred. No. 1.1e
8; Mismatches
                                                                                                                                                                                                                                                                            O-LINKED (GLYCOSAMINOGLYCAN)
SIMILARITY).
O-LINKED (GLYCOSAMINOGLYCAN)
SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                     LRR-T 4.
LRR-S 3.
LRR-T 5.
LRR-T 6.
LRR-S 4.
LRR-T 7.
                                                                                                                                                                                                                                     Score 616; DB 1;
Pred. No. 1.1e-36;
                                                                                                                                                                                                                                                                                                                                                                                                   BIGLYCAN.
CYS-RICH.
                                                                                                                                                                                                                                                                                                                                                                            LRR-S
LRR-T
LRR-T
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                            22.2
                                                                                                                                                                                                                                                                                                                                                                                                                                          Proteoglycan; Repeat;
                                                                                                                                                                                                                                            Length 272;
                                                                                                                                                                                                                                                             CRC64;
                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                             (BY
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                                                                                                                              149
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        DOMAIN
DISULFID
CARBOHYD
CARBOHYD
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CARBOHYD
                                                                                      REPEAT
REPEAT
REPEAT
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Q9EQP5;
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SIGNAL
                                                               REPEAT
REPEAT
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REPEAT
REPEAT
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                                                                                                                                                                                            Glycoprotein;
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gulfate.";
J. Biol. Chem.
-!- FUNCTION: M
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InterPro; IPR003591; LRR typ.
Pfam; PF00560; LRR; 7.
Pfam; PF01462; LRRNT; 1.
SMART; SM00013; LRRNT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a copyred the swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Prolargin precursor (Proline-arginine-rich end leucine-rich repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Biol. Chem. 275:40695-40702(2000).
- PUNCTION: May anchor basement memb connective tissue (By similarity).
-!- SUBUNIT: Binds the basement membra:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bengtsson E., Aspberg A., Heinegaard D., "The amino-terminal part of PRELP binds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Connective tissue;
MEDLINE=20576219; PubMed=11007795;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULÂR LOCATION: Secreted; extracellular matrix. DOMAIN: The basic amino-terminal Arg/Pro-rich binds hepari. heparan sulfate. Binds collagens type I and type II throug leucine-rich repeat domain (By similarity). SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SLRP) FAMILY. CLASS II SUBFAMILY.
SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: Binds the basement membrane heparan perlecan and triple helical collagens type I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF163569; AAG23724.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR001611; LRR.
                                                                                                                                                                                                                                                                                                                                                                                                           Extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
Chordata;
Rodentia;
                                                                                           POTENTIAL.
PROLARGIN
CYS-RICH.
LAR-S 1.
LAR-T 1.
LAR-T 2.
LAR-T 3.
LAR-T 3.
LAR-T 3.
LAR-S 3.
LAR-T 5.
LAR-T 6.
LAR-T 6.
LAR-T 7.
LAR-T 7.
LAR-T 7.
                                                                                                                                                                                                                                                                                                                                                                                                         matrix; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             membranes to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             377
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                                                                                                                                                                                                                                                                                                                                                                                                         Leucine-rich repeat;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sulfate proteoglycan and type II (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and
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Best Local S
Matches 96
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protein).
                                                                                                                                                                                             +
                                                                                                                                                                                                                                                   and
                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Articular cartilage;
MEDLINE=20576219; PubMed=11007795;
Bengtsson E., Aspberg A., Heinegaard D.,
"The amino-terminal part of PRELP binds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Ce
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9GKN8;
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BOVIN
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                                                                                                                                                                                                                                                                                       MEDLINE=21964083; PubMed=11847210;
Bengtsson E., Moergelin M., Sasaki
                                                                                                                                                                                                                                                                                                                                                              sulfate."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003
28-FEB-2003
                                                                                                                                                                                                                                                              "The leucine-rich
                                                                                                                                                                                                                                                                                                                        FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELP.
                                                                                                                                                                                                                      he leucine-rich repeat protein PRELP binds perlecan and d may function as a basement membrane anchor."; Biol. Chem. 277:15061-15068(2002).
- FUNCTION: May anchor basement membranes to the underly
                                                                                                                                                                                                                                                                                                                                                  Biol.
                                                                         SUBUNIT: Binds the basement membrane heparan sulfate proteoglycan perlecan and triple helical collagens type I and type II.

SUBCELLULAR LOCATION: Secreted; extracellular matrix.

DOMAIN: The basic amino-terminal Arg/Pro-rich binds heparin and heparan sulfate. Binds collagens type I and type II through its leucine-rich repeat domain.

SIMILARITY: BELONGS TO THE SWALL LEUCINE-RICH PROTEOGLYCAN (SLRP) FAMILY. CLASS II SUBFAMILY.

SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
        ween the Swiss Institute of Bioinforma
European Bioinformatics Institute. Th
by non-profit institutions as long
                                                                                                                                                                                                         connective tissue.
                                    SWISS-PROT entry is copyright. It is produced through a een the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119
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                                                                                                                                                                                                                                                                                                                                                 Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EPTDLPPPLPPG---PPSVFPDCPRECYCPPDFPSALYCDSRNLRKVP-IIPPRIHYLYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FNISNLLVLHLSHNKISNVP---AISNKLEHLYLNNNSIEKINGTQICP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTPHLRELHLDNNKLTRVPGGLAEHKYIQVVYLHNNNISVVGSSDFCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HNILRRMPPKVPPAIHOLYLDSNKIETIPSGYFKDFPNLAFIRMNYNKLS--DRGLPKNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DTNITSIPQGLPPSLTELHLDGNKISRVDAASLKGLNNLAKLGLSFNSISAVDNG---SL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QNNFITELPVESFKNATGLRWINLDNNRIRKVDQRVLEKLPGLAFLYMDKNQLEEVPSAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QNNKITEIKOGDFKNLKNLHALILVNNKISKYSPGAFTPLVKLERLYLSKNQLKELPEKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 41, Createu,
(Rel. 41, Last sequence update,
(Rel. 41, Last annotation update)
`recursor (Proline-arginine-rich en
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Bovine)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                 275:40695-40702(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata; Craniata; Vertebrata; Eutel Cetartiodactyla; Ruminantia; Pecora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 403.5; DB
Pred. No. 1.8e-2
6; Mismatches 1
                                                                                                                                                                                                                    membranes to the underlying
                                                                                                                                                                                                                                                                                       Η.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 381
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           There are no rest
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                                                                                                                                                                                                                                                                                       R., Heinegaard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            leucine-rich
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              restrictions
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d heparan
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                                     collaboration -
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OSCHERENT

ECM2 HUMAN

STANDARD;

699

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Homo sapiens (Human)

Metazoa;

Chordata;

Craniata;

Vertebrata;

Euteleostomi;

(Matrix

glycoprotein

094769;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Extracellular matrix protein 2 precursor (Mat SC1/ECM2).

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RESULT
ECM2_H
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Best Local S
Matches 95
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R SMART; SM00013; LERNT; 1.
I Glycoprotein; Extracellular m#*
Signal.
SIGNAL
CHATT
LT 25
HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
DISULFID
CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001611; LRR.
InterPro; IPR000372; LRR_Nterm
InterPro; IPR003591; LRR_typ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF163568; AAG23723.1; -.
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                                                                                                                                                                                179
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                                                                        FNISHLIVLHLSHNRISSVP---AISSRLEHLYLNNNSIEKINGTQICP
                                                                                                        ANTPHLRELHLDNNKLTRVPGGLAEHKYIQVVYLHNNNISVVGSSDFCP
                                                                                                                                            HNTLRKMPPKVPSAIHQLYLDSNRIEAIPSGYFKGFPNLAFIRLNYNQLS--DRGLPKNS
                                                                                                                                                                         DTWITSIPQGLPPSLTBLHLDGNKISRVDAASLKGLNNLAKLGLSFNSISAVDNG---SL
                                                                                                                                                                                                                                         PKTLQELRAHENEITKYRKYTFNGLNQMIVIELGTNPLKSSGIENGAFQGMKKLSYIRIA
                                                                                                                                                                                                                                                                                             QNNFITELPVESFKNATGLRWINLDNNRIRKVDQRVLEKLPSLVFLYLEKNQLEEVPAAL
                                                                                                                                                                                                                                                                                                                  QNNKITEIKDGDFKNLKNLHALILVNNKISKVSPGAFTPLVKLERLYLSKNQLKELPEKM
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                                                                                                                                                                                                                                                                                                                                                                                                       EASGIGPEVPDDRDFEPSLGPVCPFRCQC---HLRVVQCSDLGLDKVPKDLPPDTTLLDL
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N-LINKED
N-LINKED
N-LINKED
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CYS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 402.5;
Pred. No. 2.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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(GLCNAC...)
(GLCNAC...)
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1es 122;
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(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
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                                                                                                          284
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Best I
                                                                        Matches
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Nishiu J., Tanaka T., Nakamura Y.,
"Identification of a novel gene (ECM2) encoding a putative
extracellular matrix protein expressed predominantly in adipose and
femmale-specific tissues and its chromosomal localization to 9q22.3
Genomics 52:378-381(1998).

-i- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
-i- TISSUE SPECIFICITY: Expressed predominantly in adipose tissue
-i- TISSUE SPECIFICITY: Expressed predominantly in adipose tissue
                                                                                                                                                       REPEAT
DOMAIN
SITE
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                 REPEAT
REPEAT
REPEAT
REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001611; LRR. typ. InterPro; IPR003591; LRR typ. InterPro; IPR001007; VWF_C. Pfam; PF00560; LRR; 10. Pfam; PF00093; VWG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL of the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.com send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99009324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria;
                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AB011792; BAA33958.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -
                                                                                      Local
                                                                                                        Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO:0005578; C:extracellular matrix; TAS.
GO:0005178; F:integrin binding activity;
GO:0007160; P:cell_matrix adhesion; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: Contains 1 VWFC domain. SIMILARITY: Contains 12 leucine-rich (LRR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   uterus.
SIMILARITY:
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   279
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SM00214; VWC; 1.
                                     7
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                                                                                      Similarity
GEEGEEDEEDPVRGDMFRMPSRSPLPAPPRGTLRLPSGCSLSYRTISCINAMLTQIP
                                     GPEVPDDRDFE----
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                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=9790758;
T., Nakamura Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ECM2
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43206666544444375589
432067424976659
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                                                                                                                                          79789
                                                                                    22.7%;
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                                                                                                                                                 LER-S 1.

LER-T 1.

LER-T 2.

LER-T 3.

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LER-T 4.

LER-S 1.

LER-S 1.

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LER-S 1.

LER-T 5.

LER-T 6.

LER-T 7.

LER-T 7.

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LER-T 
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                                                                      58;
                                                             Score 389; ин
Pred. No. 4.3e
58; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR VWFC.
                                                                                                                                     N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
E44E76A40A5C2742 CRC6
                                -PSLGPV-----CPFRCQCHLRVVQCSDLGLDKVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (See http://www.isb-sib.ch/announce/
                                                                                    DB 1;
.3e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MATRIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Extracellular matrix;
                                                                    144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeats.
                                                                                                                                       CRC64;
                                                                                                   Length 699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN
                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEOGLYCANS
                                                                                                                                                                       (POTENTIAL)
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                                                                    104;
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                                                                  Gaps
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RESULT
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RC TISSUE-Salivary gland;
RX MEDLINE=22388257; PubMed=12477932;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gumaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,
RA Richards S., C., Steutona J.W., Green E.J., Lu X., Gibbs R.A.,
RA Rabey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Rabey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Rabey J., Helton E., Ketteman M., Macra M.A.,
RA Richards S., Sanchez R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Schein J.E.,
RA Rodriguez A.C., Schein J.S., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Schein J.S., Schmutz J., Myers R.M.,
RA Rodriguez A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2003
28-FEB-2003
15-SEP-2003
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MEDLINE=21588626;
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Mammalia; Eutheria;
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(Rel. 41, Last sequence update)
(Rel. 42, Last annotation update)
(Rel. 42, Last annotation rich en
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Rodentia;
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thi; Muridae; Murinae; Mus
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Matches 93
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SIGNAL
CHAIN
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InterPro; IPR001372; LRR. Nterm.
InterPro; IPR0013591; LRR. typ.
Pfam; PF00560; LRR; 7.
Pfam; PF01462; LRRNT; 1.
SMART; SM00013; LRRNT; 1.
SMART; SM00013; LRRNT; 1.
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EMBL; AF261887; AAF72994.2;
EMBL; BC019775; AAH19775.1;
                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            developing embryo prior to skeletogenesis. In adult, highest expression in lung, lower levels in cardiac and skeletal muse DOMAIN: The basic amino-terminal Arg/Pro-rich binds heparin heparan sulfate. Binds collagens type I and type II through leucine-rich repeat domain (By similarity).

SIMILARITY: BELONGS TO THE SWALL LEUCINE-RICH PROTEOGLYCAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         perlecan and triple helical collagens type I and type similarity).
SUBCELLULAR LOCATION: Secreted; extracellular matrix.
TISSUB SPECIFICITY: Expressed in cartilage throughout
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Contains 12 leucine-rich (LRR) repeats
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                                 119
                                                                106
 166
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                                                                               QNNKITEIKDGDFKNLKNLHALILVNNKISKVSPGAFTPLVKLERLYLSKNQLKELPEKM
PRNLEQLELSQNLISRIPPGVFSKLENLLLLLDLQHNRLSDGVFKADTFQGLKNLMQLNLA
                                                             QNNFITELPLESFQNATGLRWVNLDNNRIRKVDQRVLGKLPSLAFLYMEKNQLEEVPSAL
                                                                                                                                                        EASGIGPEVPDDRDFEPSLGPVCPFRCQC---HLRVVQCSDLGLDKVPKDLPPDTTLLDL
                               PKTLQELRAHENE I TKVRKVT FNGLNQMI VI ELGTNPLKSSG I ENGAFQGMKKLSYI RI A
                                                                                                                            EPTDLPPPLPPG---PPSVFPDCPRECYCPPDFPSALYCDSRNLRRVPV-IPPRIHYLYL 105
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                                                                                                                                                                                                                                                        378
                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
PROLARGIN.
CYS-RICH.
LRR-S 1.
LRR-T 1.
LRR-T 2.
LRR-S 2.
LRR-T 3.
LRR-T 4.
LRR-T 4.
LRR-S 3.
LRR-T 5.
LRR-T 6.
LRR-S 1.
LRR-T 7.
LRR-S 1.
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                                                                                                                                                                                                         Score
Pred.
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LRR-T 1.
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(POTENTIAL).
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RX MEDLINE=2238257; PhuMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Biotchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Biotchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Rodriguez A.C., Grimcood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Rodriguez A.C., Grimcood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA FUNCTION. Mag anchor basement membrane heparan sulfate proteoglycan C.
- FUNCTION: May anchor basement membrane heparan sulfate proteoglycan C.
- Connective tissue (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1996
01-OCT-1996
15-SEP-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE=Pancreas, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Grover J., Chen X.-N., Korenbe
"The gene organization, chromc
55-kDa matrix protein (PRELP)
Genomics 38:109-117(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=97127584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=96029653; PubMed=7592739;
Bengtsson E., Neame P.J., Heinegaard D., Sommarin Y.;
"The primary structure of a basic leucine-rich repeat
found in connective tissues.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRLP
                         <u>-</u>
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heparan sulfate. Binds collagens type I and type leucine-rich repeat domain (By similarity).

SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PRO (SLRP) FAMILY. CLASS II SUBFAMILY.
                                                      SUBCELLULIAN ACCOUNTS TISSUE SPECIFICITY: Connective tissue.

DOMAIN: The basic amino-terminal Arg/Pro-rich binds heparin DOMAIN: The basic amino-terminal type I and type II through
                                                                                                                       SUBCELLULAR LOCATION: Secreted; extracellular
                                                                                                                                          perlecan and triple helical
similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAMOH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   226
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(Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and
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42,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Korenberg J.R., Recklies, chromosome location, and (PRELP) of human articular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                        membrane heparan sulfate collagens type I and type
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .R., Recklies A.D., Roughley
location, and expression of
uman articular cartilage.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                382
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                         PROTEOGLYCAN
                                                                                                                                                               type
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e II (By
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Query Match
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Matches 91
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Signal; Polymo
SIGNAL
CHAIN 2
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GO; GO:0005201; F:extracellular matrix structural (GO; GO:0005501; P:skeletal development; TAS.
InterPro; IPRO01611; LRR.
InterPro; IPR000372; LRR_Nterm.
Pfam; PF00560; LRR; 8.
Pfam; PF00560; LRR; 1.
SMART; SM00013; LRRNT; 1.
Glycoprotein; Extracellular matrix; Repeat; Leucin
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DISULFID
CARBOHYD
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CARBOHYD
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EMBL; U41344; AAC18782.1; -.
EMBL; U41343; AAC18782.1; JOINED.
EMBL; BC032498; AAH32498.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
                                                                                                                                                                                                                                                                                                                  SEQUENCE
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REPEAT
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PIR; I39068;
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                                                                                                                                                                                                                                                                                                                                              VARIANT
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Genew; HGNC:9357; PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
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                             230
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                                                                                                                                                                                                                                                            91;
                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polymorphism
 ANTPHLRELHLDNNKLTRVPGGLAEHKYIQVVYLHNNNISVVGSSDFCP
                                                     DTNITSIPQGLPPSLTELHLDGNKISRVDAASLKGLNNLAKLGLSFNSISAVDNG---SL
                                                                                                  PKTLQELRAHENEITKVRKVTFNGLNQMIVIELGTNPLKSSGIENGAPQGMKKLSYIRIA
                                                                                                                                          QNNFITELPVESFQNATGLRWINLDNNRIRKIDQRVLEKLPGLVFLYMEKNQLEEVPSAL
                                                                                                                                                       QNNKITEIKDGDFKNLKNLHALILVNNKISKVSPGAFTPLVKLERLYLSKNQLKELPEKM
                                                                                                                                                                                               EPTDLPPPLPPG---PPSIFPDCPRECYCPPDFPSALYCDSRNLRKVPV-IPPRIHYLYL
                                                                                                                                                                                                                          EASGIGPEVPDDRDFEPSLGFVCPFRCQC---HLRVVQCSDLGLDKVPKDLPPDTTLLDL
                          HNILRKMPPRVPTAIHQLYLDSNKIETIPNGYFKSFPNLAFIRLNYNKLT--DRGLPKNS
                                                                                 PRNIEQLRLSQNHISRIPPGVFSKLENLLLLDLQHNRLSDGVFKPDTFHGLKNLMQLNLA
                                                                                                                                                                                                                                                                                                                  382
                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                             139
139
                                                                                                                                                                                                                                                                                                                AA;
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                                                                                                                                                                                                                                                                                                                                              43809 MW;
                                                                                                                                                                                                                                                        22.5%; Score 385.5; DB 1
31.5%; Pred. No. 3.4e-20;
live 59; Mismatches 124
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N-LINKED (GLCNAC...) (I

N-LINKED (GLCNAC...) (I

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N-H (IN dbsnp:9439).

/FTId=VAR_011976.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
PROLARGIN.
CYS-RICH.
LURR-S 1.
LURR-T 1.
LURR-T 2.
LURR-S 2.
LURR-S 3.
LURR-T 4.
LURR-S 3.
LURR-T 5.
LURR-T 6.
LURR-S 17.
LURR-S 7.
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                                                                                                                                                                                                                                                                                                                A1C4E166B7515695 CRC64;
                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                         124;
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                                                                                                                                                                                                                                                         Indels
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                    382;
284
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     Matches
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1_RABIT
PGS1_RABIT
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28-FEB-2003
28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99037997; PubMed=9822203;
Boykiw R.H., Sciore P., Reno C.R., Marchuk L., Fra
"Altered levels of extracellular matrix molecules
                                                                                                                                                                                                                                                                             Giycoprotein;
                                                                                                                                                                                                                                                                                                                                                 EMBL; AF020290; AAC39515.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity).
-i- SUBUNIT: Forms a ternary complex with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rabbit ligaments.";
Matrix Biol. 171:371-378(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                         Leuci
                                                                                                                                                                                                                                                                                             Pfam; PF00560; LRR; 4.
                                                                                                                                                                                                                                                                                                               InterPro; IPR001611;
InterPro; IPR003591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryctolagus cuniculus (Rabbit).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- FUNCTION: May be involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=New Zealand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: Contains at least 6 leucine-rich (LRR) repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity).
TISSUE SPECIFICITY: Found in several connective tissues,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 288
                                                                                                                                                                                                                                                         le-rich
     . Similarity 72; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FNISNLLVLHLSHNRISSVP---AINNRLEHLYLNNNSIEKINGTQICP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Bone/cartilage
                                                                                 135
       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 41, Created)
(Rel. 41, Last sequence up
(Rel. 41, Last annotation
one/cartilage proteoglycan
                                                                                                                                         16
37
85
                                                                                                                                                                                                                                                     repeat.
                                                                                                                                                                                                                                                                       Extracellular matrix; Proteoglycan; Repeat;
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                       54.5%;
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   24;
                       Score
Pred.
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28-FEB-2003
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-!- SUBUNIT: Binds to laminin (By similarity).

-!- SUBUNIT: No INCANTON: Secreted; extracellular matrix
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                        CHAIN
DOMAIN
REPEAT
                                                                                                                                                 Pfam; PF00560; LRR; 10.
Pfam; PF01462; LRRNT; 10.
PRINTS; PR00019; LEURICHRPT.
SMART; SM00369; LRR TYP; 1.
SMART; SM00013; LRRNT; 1.
                                                                                                                                                                                                                                                                                       This
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coturnix coturnix japonica (Japanese quail).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Archosauria, Aves, Neognathae, Galliformes, Phasian
                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20556471;
                                                                                                                            SIGNAL
                                                                                                                                            Glycoprotein;
                                                                                                                                                                                                            EMBL; AF125251; AAG48155.1; -. InterPro; IPR001611; LRR.
                                                                                                                                                                                                                                               entities
                                                                                                                                                                                                                                                       modified
                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Cornea;
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                Coturnix.
NCBI_TaxID=93934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lumican precursor
                REPEAT
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Matrix Biol. 19:699-704(2000)
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                                                                                                                                                                                                                                                                                                      PTW: Binds keratan sulfate chains (By similarity).
SIMILARITY: BELONGS TO THE SWALL LEUCINE-RICH PROTE
(SIRP) PAMILY. CLASS II SUBFAMILY.
SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
                                                                                                                                                                                                                                                             European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
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                                                                                                                                   repeat;
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LUMICAN.
CYS-RICH.
LRR-S 1.
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LRR-T 4.
LRR-T 4.
LRR-T 5.
LRR-T 6.
LRR-T 6.
LRR-T 9.
LRR-T 10.
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Phasianidae; Phasianinae;
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SEQUENCE
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 SEQUENCE FROM N.A.
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                                         Hassell J.R.;
                                                                  TISSUE=Cornea
                                                                          SEQUENCE
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Similarity
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GPLTYSKITHLRLDGNNLTRADLPQEMYNCLRVAAEISL
                                                     -DSGIPGNVFNITSLVELDLSFNQLKSIP---TVSENLENFYLQVNKINKFPLSSFCKVV
                                                                                                           NSLLYLDLSFNOLTKLPTGLPHSLLMLYFDNNQISNIPDEYFQGFKTLQYLRLSHNKLT-
                                                                                                                                      KKLSYIRIADTNITSIPQGLPPSLTELHLDGNKISRVDAASLKGLNNLAKLGLSFNSISA
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                                                                                                                                                                                                                                                                                                          SGI-----GPEVPDDRDFEPSLGP---VCPFRCQCHL---RVVQCSDLGLDKVPKDLPP
                        HNTKKASYSGVSLFSNPVQYWEIQPSTFRCVYVRSAIQL
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                                                                                                                                                                                                                                                                                                                                      58;
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N-LINKED (GLCNAC.
(POTENTIAL).
N-LINKED (GLCNAC.
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(POTENTIAL).
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Pred. No. 5.
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P51884; Q96QM7;
01-OCT-1996 (Rel
28-FEB-2003 (Rel
                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996 (Rel. 3
28-FEB-2003 (Rel. 4
15-SEP-2003 (Rel. 4
Lumican precursor (
                                                                                                                                    SEQUENCE FROM N.A.
TISSUE=Cartilage, Intestine, and Placer
MEDLINE=95394964; PubMed=7665616;
Grover J., Chen X.-N., Korenberg J.R.,
"The human lumican gene. Organization,
expression in articular cartilage.";
J. Biol. Chem. 270:21942-21949(1995).
                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
              "Primary structure and localization or
                                                           MEDLINE=96047334;
Chakravarti S., S
                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
27:481-488 (1995)
                                                                                                         N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                           Stallings
                                                                                                                                                                                                                                                                                                                                                                 . 34, Creat
. 41, Last
. 42, Last
r (Keratan
                                                                           PubMed=7558030;
                             of human lumican
                                                                                                           AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                   Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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Last
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                gene
                                                         R.L.,
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annotation update)
sulfate proteoglycan
              (MUT)
                                                                                                                                                                                                                      and Placenta;
                                                         Sundarraj N.,
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                             (keratan sulfate
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                chromosome
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                                                              Cornuet
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             fate proteoglycan)
12q21.3-q22.";
                                                                                                                                                                          location,
                                                              P.K.,
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                                                                                                                                                                        and
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TISSUE=Prostate; MEDLINE=22388257; PubMed=12477932;

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InterPro; IPR001611; LRR.
InterPro; IPR000372; LRR Nterm.
InterPro; IPR003591; LRR typ.
Pfam; PF00160; LRR; 9.
Pfam; PF01462; LRRNT; 1.
PRINTS; PR00019; LEURICHRPT.
                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-gorsend an email to license@@isb-sib.ch).
   REPEAT
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SMART; SM00369; LER TYP; 1.
SMART; SM00013; LERNT; 1.
Glycoprotein; Extracellular matrix; Proteoglycan;
                                                                                                                                                                                                                                                                                                            EMBL; U18728; AAA85268.1; -.
EMBL; U21128; AAA91639.1; -.
EMBL; BC007038; AAH07038.1; -.
                                                                                                                                                                                                                                                  MIM, 600616; -.
GO; GO:0005578; C:extracellular
GO; GO:0005203; F:proteoglycan;
GO; GO:0007601; P:vision; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SLRP) FAMILY. CLASS II SUBFAMILY.
-!- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
                                                                                                      DOMAIN
                                                                                                                             SIGNAL
                                                                                                                                                                                                                                                                                                    Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEVELOPMENTAL STAGE: Present in the extracellular matrix of human articular cartilage at all ages, although its abundance is far greater in the adult. In the adult cartilage lumican exists predominantly in a glycoprotein form lacking keratan sulfate, whereas the juvenile form of the molecule is a proteoglycan. SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity).
TISSUE SPECIFICITY: Cornea and other tissues.
DEVELOPMENTAL STAGE: Present in the extracell
                                                                                                                                                                                                                                                                                                   HGNC:6724; LUM.
                                                                                                                                        repeat;
  338
53
78
102
128
149
171
171
217
241
                                                                                                                                      Signal.
BY SIMILAL LIMICAN.
CYS-RICH.
LTR-S 1.
LTR-T 1.
LTR-T 2.
LTR-T 2.
LTR-T 3.
LTR-T 3.
LTR-T 4.
LTR-T 5.
LTR-T 5.
                                                                                                                                                                                                                                                                TAS.
                                                                                                                            SIMILARITY.
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                                                                                                                                                                                                                                                        Similarity
                                                                                                                     ELRAHENEITKVRKVTFNGLNOMIVIELGTNPLKSSGIENGAFQGMKKLSYIRIADTNIT
:|: ||: ||: ||: :: |
DLQLTHNKITKLG--SFEGLVNLTFIHLQHNRLKEDAV-SAAFKGLKSLEYLDLSFNQIA
                                                                                                  SIPQGLPPSLTELHLDGNKISRVDAASLKGLNNLAKLGLSFNSISAVDN----GSLANTPH
                                                                                                                                                                                                                         DRDFEPSL----GPVCPFRCQC---HLRVVQCSDLGLDKVPKDLPPDTTLLDLQNNKITE
KHLRLDGNRISETSLPPDMYECLRVANEVTL
                    S---LFSNPVQYWEIQPSTFRCVYVRSAIQL
                                                                               RLPSGLPVSLLTLYLDNNKISNIPDEYFKRFNALQYLRLSHNELA--DSGIPGNSFNVSS
                                                                                                                                                                        IKOGDEKNIKNIHALIIVNNKI--SKVSPGAFTPLVKLERLYLSKNQLKELPEKNPKTLQ | : |:|::| | | | :|:|::|
                                                                                                                                                                                                     DYDFPLSIYGQSSPNCAPECNCPESYPSAMYCDELKLKSVPM-VPPGIKYLYLRNNQIDH
                                       LVELDLSYNKLKNIP----TVNENLENYYLEVNOLEKFDIKSFCKILGP----
                                                            LRELHLDNIKLTRVPGGLAEHKYIQVVYLHNINISVVGSSDFCP---PGHNTKKASYSGV
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LRR-T 7.
LRR-T 8.
BY SIMILARITY.
THKED (GLCNAC...
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(POTENTIAL).
L -> V (IN REF. 1).
L -> V (IN REF. 1).
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7; Mismatches 135
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RA Strausberg R.D., Felmpold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetcw K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Robask S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J.M., Warra M.A.;
Ra Rodriguez A.C., Grimwood J., Schmutz J.M., Warra M.A.;
Ra Rodriguez A.C., Grimwood J., Schmutz J.M., Warra M.A.;
Ra Rodriguez A.C., Grimwood J., Schmutz J.M., Warra M.A.;
Ra Rodriguez A.C., Grimwood J., Schmutz J.M., Warra M.A.;
Ra Rodriguez A.C., Grimwood J., Schmutz J.M.,
Ra Rodriguez A.C., Grimwood J., Schmutz J.M.,
Ra Rodriguez A.C., Scholl J.S.A., Policies A.C., Grimwood J., Schmutz J.M.,
Ra Rodriguez A.C., Scholl J.S.A., Policies A.C., Scholl J.S.A., Policies A.C., Scho

Search Job tim time completed: February , 2004, 11:36:34

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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*
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9: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*
10: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*
11: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*
12: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*
13: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*
14: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*
15: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:*
16: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:*
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696.281 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

9	œ	7.	6	IJ	4	w	2	_	Result
1628	1653	1704	1709	1709	1709	1709	1709	1709	Score
95.0	96.5	99.5	99.8	99.8	99.8	99.8	99.8		Query Match
347	353	342	1388	1388	360	359	359	331 14	Query Match Length DB
24	1	17	21	17	22	22	21	14	DB
AAE34392	AAR05160	AAR89439	AAY84539	AAR89471	AAU87286	AAG78511	AAY57079		ID
Human decorin prot	Sequence of human	Human recombinant	Amino acid sequenc	Collagen/decorin f	Novel central nerv	Human decorin amin	Human decorin amin	Mature decorin PT-	Description

4.4 5	43	42	41	40	39	38	37	36	35	34	33	3 2	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10
742.5 735	925.5	•	•	٠	•	•	•	•	943.5		•	•	•	•	•	•	•	•	•	•	943.5	948	965	966	976.5	J	979 .	979	979	979	985.5	1186	1429	1567
43.3	•	•	•	•	•	•	55.1	55.1	55.1	55.1	55.1	55.1	55.1	55.1	55.1	55.1	55.1	55.1	55.1	55.1	•	•	56.3	•	•		•	57.2	•	•	•	•	•	•
423 146	373	373	352	379	344	379	379	379	379	379	379	379	379	379	379	379	379	379	379	379	379	186	368	368	332	369	368	368	368	368	369	234	280	305
22 20	23	22	22	20	22	24	24	24	24	24	24	24	24	24	24	24	24	23	23	22	21	14	11	22	16	16	24	24	24	22	16	14	14	14
AAU30348 AAY59749	ABB72356	4	ABG22569	N	AAM40351	ABU11302	ABU57236	ABU56301	ABU55920	ABU58350	4	ABU60230	ABU64916	ABU59814	ABU67121	ABU67009	ABU66733	ABB84831	ABB95437	AAU12335	AAB01311	AAR42264 .	AAR05159	AAG78510	AAR87953	AAR87952	AAE34394	ABR47399	ABR39564	AAB85043	AAR87951	AAR42265	AAR42266	AAR42267
Novel human secret Human normal ovari		Mouse bone/cartila				Human pro241 prote	Human PRO241 prote	Human secreted/tra	-		Novel human secret	Human PRO polypept	Human secreted/tra	Novel secreted and	PRO poly	Human secreted/tra	PRO pol		Human angiogenesis		Human PRO241 polyp		3	Human biglycan ami	Bovine neurotrophi	Human neurotrophic	Human biglycan pro	Breast cancer asso	Human biglycan pro	Human biglycan pro	Rat neurotrophic b		sequence	Decorin sequence P

## ALIGNMENTS

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WO9320202-A1. 14-OCT-1993.		kegion 281331 /label= C-terminal_region			/note= "contains 4 Cys residues"		Region 145 .	Key Location/Qualifiers		Bos sp.	decorin; PG-II; PG-40; transforming growth factor-beta; TGF-beta.		leucine-rich repeat; proteoglycan; cell regulatory factor; MBP;		Mature decorin PT-65.		28-APR-1994 (first entry)	09-JAN-2003 (updated)	25-MAR-2003 (updated)		AAR42260;		AAR42260 standard; Protein; 331 AA.	AAR42260	TOT 1

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RESULT 2
AAYS709
ID AAYS7
XX
AC AAXS
XX
DT 28-F
XX
KW Negl
KW Negl
KW inmult
KW mult
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XX
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Active fragments of decorin (full-length coding sequence AAQ50046) were generated by PCR and fused to Maltose Binding Protein. The resulting fusion proteins were useful for inhibiting the activity cacell regulatory factor, esp. TGF-beta, and hence for treating conditions associated with over-activity of the growth factor such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Active factor
           Neglected target tissue antigen; NTTA; autoimmunity; autoimmune response; immunotherapeutic agent; insulin dependent diabetes mellitus; multiple sclerosis; autoimmune thyroiditis; rheumatoid arthritis; uveoretinitis; inflammatory response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cardenas J,
Ruoslahti EI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                               Human
                                                                                                        28-FEB-2000
                                                                                                                                   AAY57079
                                                                                                                                                            AAY57079 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
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DB; AAQ50046.
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                                                                                                                                                                                                                                                                                                RELHLDNNKLTRVPGGLAEHKYIQVVYLHNNNISVVGSSDFCPPGHNTKKASYSGVSLFS
                                                                                                                                                                                                                                                                                                                                                   TTSTPQGLPPSLTELHLDGNKTSRVDAASLKGLNNLAKLGLSFNSTSAVDNGSLANTPHL
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                                                                                                                                                                                                                                                                                RELHLDNNKLTRVPGGLAEHKYIQVVYLHNNNISVVGSSDFCPPGHNTKKASYSGVSLFS
                                                                                                                                                                                                                                                                                                                                     ITSIPQGLPPSLTELHLDGNKISRVDAASLKGLNNLAKLGLSFNSISAVDNGSLANTPHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 36-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.8%; So ilarity 100.0%; 1 Conservative 0;
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                                                                            acid sequence.
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                                                                                                                                                            359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1709; DB 14;
Pred. No. 3.6e-145;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tissue antigens NTTAs. NTTAs are antigens (whole antigens or fragments)
continvolved in autoimmunity. These peptides and proteins are used in
the method of the invention which involves administering an NTTA as an
antigen based immunotherapeutic agent, to a host afflicted with an
autoimmune response associated with an autoimmune disease. The
immunotherapeutic agent is used to treat autoimmune diseases such as
insulin dependent diabetes mellitus, multiple sclerosis, autoimmune
thyroiditis, uveoretinitis, rheumatoid arthritis or abnormal
inflammatory immune responses. The NTTA induces regulatory tolerance by
elicitation of regulatory T cells among T cells recognizing the NTTA but
not participating in the immune response . The NTTA are capable of
recognition by substantial populations of uncommitted T cells which can
be primed, or biased, towards regulatory responses to provide effective
treatment. The NTTA are effective in regulating undesirable immune
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                responses even when target determinants used as agents promoting tolerance agents have failed to induce an effective regulatory Tresponse. NTTAs as agents promoting tolerance are anticipated to than use of target determinants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kaufman DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use of target
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332
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                                                                                                                                                                                                                                                                       92
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                              NPVQYWEIQPSTFRCVYVRSAIQLGNYK 329
                                                                                 RELHLDNNKLTRVPGGLAEHKYIQVVYLHNNNISVVGSSDFCPPGHNTKKASYSGVSLFS
                                                                                                                                   ITSIPQGLPPSLTELHLDGNKISRVDAASLKGLNNLAKLGLSFNSISAVDNGSLANTPHL
                                                                                                                                                       ITSIPQGLPPSLTELHLDGNKISRVDAASLKGLNNLAKLGLSFNSISAVDNGSLANTPHL
                                                                                                                                                                                                       LQELRAHENEITKVRKVTFNGLNQMIVIELGTNPLKSSGIENGAFQGMKKLSYIRIADTN
                                                                                                                                                                                                                         LQELRAHENEITKVRKVTFNGLNQMIVIELGTNPLKSSGIENGAFQGMKKLSYIRIADTN
                                                                                                                                                                                                                                                                       KITEIKDGDFKNLKNLHALILVNNKISKVSPGAFTPLVKLERLYLSKNQLKELPEKMPKT
                                                                                                                                                                                                                                                                                          KITEIKDGDFKNLKNLHALILVNNKISKVSPGAFTPLVKLERLYLSKNQLKELPEKMPKT
                                                                                                                                                                                                                                                                                                                                         EASGIGPEVPDDRDFEPSLGPVCPPRCQCHLRVVQCSDLGLDKVPKDLPPDTTLLDLQNN
                                                                                                                                                                                                                                                                                                                                                                  EASGIGPEVPDDRDFEPSLGPVCPFRCQCHLRVVQCSDLGLDKVPKDLPPDTTLLDLQNN
                                                                 RELHLDNNKLTRVPGGI
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                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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100.0%; Pred. No. 4e-145;
tive 0; Mismatches 0
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271 241 211 181 151 91

121

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328; Conservative

Best Local Similarity

100.0%;

<u>,</u>

Pred. No. 4e-145; ; Mismatches 0;

Indels

0

Gaps

0

S 밁 á 묽 ð

LQELRAHENEITKVRKVTFNGLNQMIVIELGTNPLKSSGIENGAFQGMKKLSYIRIADTN

181 151

LQELRAHENE I TKVRKVT FNGLNQM I VI ELGTNPLKSSG I ENGAFQGMKKLSY I R I ADTN

KITEIKOGDFKNLKNLHALILVNNKİSKVSPGAFTPLVKLERLYLSKNQLKELPEKMPKT KITEIKDGDFKNLKNLHALILVNNKISKVSPGAFTPLVKLERLYLSKNQLKELPEKMPKT 121

ITSIPQGLPPSLTELHLDGNKISRVDAASLKGLNNLAKLGLSFNSISAVDNGSLANTPHL

 ${\tt ITSIPQGLPPSLTELHLDGNKISRVDAASLKGLNNLAKLGLSPNSISAVDNGSLANTPHL}$ 

62

32 EASGIGPEVPDDRDFEPSLGPVCPFRCQCHLRVVQCSDLGLDKVPKDLPPDTTLLDLQNN

91

61

EASGIGPEVPDDRDFEPSLGPVCPFRCQCHLRVVQCSDLGLDKVPKDLPPDTTLLDLQNN

S 밁 δ 밁 Ś B

302 272 242 212 182 152 122 92

NPVQYWEIQPSTFRCVYVRSAIQLGNYK 329

NPVQYWEIQPSTFRCVYVRSAIQLGNYK 359

RELHLDNNKLTRVPGGLAEHKY I QVVY LHNNN I SVVGSSDFCPPGHNTKKASYSGVSLFS

301

331

241 211

271

RELHLDNNKLTRVPGGLAEHKYIQVVYLHNNNISVVGSSDFCPPGHNTKKASYSGVSLFS

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332

AAU87286 standard; Protein; 360 AA

Novel central nervous system protein #196.

05-JUN-2002

(first entry)

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The invention relates to the inhibition of transforming growth CC factor-beta (TGF-beta) activity involving contacting TGF-beta with a CC purified polypeptide comprising leucine-rich amino acid sequence of a CC member of decorin superfamily of mammalian proteoglycans. The following CC activities can be attributed to the polypeptide of the invention: CC cytostatic, nephrotropic, antirheumatic, antiarthritic, vasotropic, CC antiarteriosclerotic, hepatotropic, cardiant, dermatological and CC vulnerary. Polypeptides of the invention act as transforming growth CC factor-beta (TGF-beta) binder. The polypeptides of the invention can be CC used for treating a pathology, particularly proliferative pathology caused by a transforming growth factor-beta (TGF-beta) regulated CC clisease, glomerulonephritis, rheumatoid arthritis, arteriosclerosis, attributory distress syndrome, carrhosis of liver, fibrosis of lungs, post-myocardial infarction, cardiac fibrosis, post-angioplasty crestenosis, renal interstitial fibrosis and certain dermal fibrotic conditions such as keloids and scarring resulting from burn injuries; other invasive skin injuries and reconstructive surgery. The wounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-NOV-1991;
17-NOV-1992;
08-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nephrotropic; Antirheumatic; Antiarturation; Cardiant; Dermatological; Antiarteriosclerotic; Hepatotropic; Cardiant; Dermatological; Glomerulonephritis; Rheumatoid arthritis; Arteriosclerosis; Adult respiratory distress syndrome; Cirrhosis; Cancer; Fibrotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG78511 standard; protein; 359 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human decorin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG78511;
                                                   other invasive skin injuries and reconstructive surgery. The wounds treated with the polypeptide, particularly decorin exhibit no detectable scarring, and are histologically normal. The current sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-610491/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-JUN-1988;
22-JAN-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BURN-) BURNHAM INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             decorin or biglycan polypeptide for inhibiting TGF-beta activity treatment of dermal wounds and cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transforming growth factor-beta; Burn; Wound; Cytostatic; ic; Antirheumatic; Antiarthritic; Vasotropic; Vulnerary
                                                                                                                                                                                                                                                                                                                                                                                                                          Fig 11; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Decorin; Biglycan; Proteoglycan; Extracellular matrix;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91US-0792192.
92US-0978931.
94US-0303238.
88US-0212702.
90US-0467888.
92US-0882345.
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31..359
/label= Mature_human_decorin
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ARESULT 4
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ARUSIZE 6
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additive;

preservative; gene

therapy

WO200155318-A2 Homo sapiens. Central nervous system; CNS; autoimmune disease; rheumatoid arthritis; hyperproliferative disorder; neoplasm; cardiavascular disorder; cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; AIDS; ocular disorder; acquired immunodeficiency virus; dysphagia; gastrointestinal disorder; adenocarcinoma; reproductive system disorder; testicular feminisation; endocrine disorder; diabette; cancer; leukaemia; neovascularisation; respiratory disorder; renal disorder; kidney failure; blood disorder; myocardial infarction; wound healing; cell proliferation; skin aging; food addition; food recorration.

Query Match

99.8%;

Score 1709;

멂 22;

Length 359;

07-JUN-2000; 28-JUN-2000;

19-MAY-2000; 18-APR-2000; 16-MAR-2000; 17-MAR-2000; 02-MAR-2000;

2000US-0186350 2000US-018974 2000US-0190076 2000US-0198123 2000US-0205515 2000US-0209467 2000US-0216847

2000US-0216880 2000US-0217487

04-FEB-2000; 24-FEB-2000;

2000US-0180628 2000US-0184664

31-JAN-2000; 2000US-0179065 17-JAN-2001; 2001WO-US01332

Sequence

359

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08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
17-NOV-2000;
17-NOV-2000;
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01-DEC-2000
The invention describes an isolated nucleic acid molecule (I) encoding a novel central nervous system protein. (I) and polypeptides (III) encoded by (I), are used to treat a medical conditions and in diagnosis of a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease and amylotrophic lateral sclerosis, infections caused by bacteria, viruses e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders e.g. coronal infection, gastrointestinal disorders e.g. dysphagia, adenocarcinomas and irritable bowel syndrome, reproductive system
                                                                                                                                                                                                                                                            WPI; 200
N-PSDB;
                                                                                                                                                                                                     New isolated nucleic acid encoding a protein for diagnosing, preventing, treating or ameliorating medical conditions and used food additives or preservatives -
                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                                (HUMA-)
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DB; ABK43616.
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2000US-0249216

2000US-0249216

2000US-0249218

2000US-0249245

2000US-0249264

2000US-0249264

2000US-0249264

2000US-0249297

2000US-0249297

2000US-0249299

2000US-0251010

2000US-0251010

2000US-02511030

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2000US-0245525.
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2000US-0246526.
2000US-0246528.
2000US-0246533.
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2000US-0249207.
2000US-0249208.
2000US-0249209.
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2000US-0246611.
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2000US-0246477.
2000US-0246478.
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2000US-0246476.
2000US-0246477.
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                                                                                                                                                                                                                                                                                                                                GENOME
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                                                                                                                                                                                                                                                                                                     XS.
                                                                                                                                                                             English.
                                                                               disorders
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26-JUL-2000
14-AUG-2000
11-AUG-2000
11-SEP-2000
11-SEP

2000US-0235484.

234998.

3-0235836. 3-0236327. 3-0236367.

200005-0229509

0-OCT-2000; 0-OCT-2000; 0-OCT-2000; 0-OCT-2000; 0-OCT-2000; 0-OCT-2000; 10-OCT-2000; 11-NOV-2000;

3-0236368 -0236369 -0236370 -02363703 -0237039 -0237039 -0237039 -0237039 -0237039 -0247020

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RESULT 5
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                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1996
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                                       11-DEC-1995
                                                                                                       CA2151547-A
                                                                                                                                                                                                                                                                           Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
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                                                                                                                                                                                                                                                                           /label=
887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tissue repair; fusion protein.
                                                                                                                                                                       note=
                                                                                                                                                                                                                                                                                                                                    /label= Linker_peptide
|060..1388
                                                                                                                                                                                                                                                                                                                                                                                                           1058..1059
                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Collagen-IA
/note= "collagen IA alpha-helical domain"
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                                                                                                                                                                                                                                       note= "unidentified amino acid"
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100.0%; Pred. No. 4e-145;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A fusion protein (AAR89471) comprises the alpha-helical region of human collagen I(a) linked to human dermatan sulphate proteoglycan (decorin). It can be expressed in Escherichia coli transformants carrying a vector incorporating a chimeric gene (AART16517) coding f the fusion. The decorin binds to type I collagen and thus affects Elbril formation.—It Thibits the cell attachment-promoting activity of collagen and fibrinogen by binding to such molecules near their cell binding sites. The collagen moiety provides an integral substratum or scaffolding for the decorin. The fusion protein acts to reduce scarring of healing tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimaeric DNA encoding protein contg. extracellular matrix protein domain - and cellular regulatory factor domain, partic. useful as osteogenic agents, also related vectors, transformed cells and
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Extracellular matrix protein; self aggregation; hydroxylated proline; trans-4-hydroxyproline; 3-hydroxyproline; recombinant protein product collagen; fibrinogen; fibronectin; post translational hydroxylation;

Amino acid sequence of a chimeric collagen 1 (alpha1)/decorin protein.

25-JUL-2000

(first

entry)

AAY84539

standard;

Protein;

decorin;

chimera.

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The specification describes a method for producing an extracellular comatrix protein or its fragment. The extracellular matrix protein is capable of self aggregating in a cell which does not ordinarily comprises optimising a nucleic acid sequence for expression in the cell by substitution of codons preferred by that cell for naturally occurring codons not preferred by the cell; corporating the nucleic acid sequence into the cell; and contacting contact acid, selected from the group consisting of trans-4-hydroxyproline and contacting containing at least one amino cacid, selected from the group consisting of trans-4-hydroxyproline and contacting containing at least one amino cacid, selected into the cell and incorporated into the extracellular matrix protein. The method may be used to make host cells assimilate and contactine into proteins. This is especially useful in the recombinant production of proteins. This is especially containing and fibronectin whose ability to self aggregate and produce functional proteins depends on the post translational hydroxypation of proteins trans-4-hydroxyproline. The method is also useful in studying the structure and function of proteins which do not normally contain trans-4-hydroxyproline.

The present sequence represents a chimeric collagen 1 (alpha1)/decorin
                                                                                                                                                                                                                                                                       Production of extracellular matrix proteins containing 4-trans-hydroxyproline results in native self aggregating proteins, useful on medical implants -
                                                                                                                                                                                                                                               Claim 25; Fig 17A-B; 260pp; English.
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                                                                                                                                                                                                                                                                                                                                                           Gruskin EA,
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                                                                                                                                                                                                                                                                                                                                                          Connolly K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCC"
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RESULT 7
AARB9JAT 7
AARB9 JID AARB
XX AARB
AC AARB
XX DACC
XX COC

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Best Local
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                                                                                      Purificn. of human recombinant exchange resin, a hydrophobic i
                                                                                                                                                                                                                                     Craig WS,
Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                      08-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                   07-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human recombinant decorin.
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                                                                strong anion exchange resin
                                                                                                                                                             N-PSDB; AAT10741.
                                                                                                                                                                                      WPI; 1996-097586/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W09601842-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Decorin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR89439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR89439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                          (LJOL-) LA JOLLA CANCER RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KITEIKDGDFKNLKNLHALILVNNKISKVSPGAFTPLVKLERLYLSKNQLKELPEKMPKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PG-II;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NPVQYWEIQPSTFRCVYVRSAIQLGNYK 1388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TSIPQGLPPSLTELHLDGNKISRVDAASLKGLNNLAKLGLSFNSISAVDNGSLANTPHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EASGIGPEVPDDRDFEPSLGPVCPFRCQCHLRVVQCSDLGLDKVPKDLPPDTTLLDLQNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    which may be produced using the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RELHLDNNKLTRVPGGLAEHKYIQVVYLHNNNISVVGSSDFCPPGHNTKKASYSGVSLFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RELHLDNNKLTRVPGGLAEHKYIQVVYLHNNNISVVGSSDFCPPGHNTKKASYSGVSLFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ITSIPQGLPPSLTELHLDGNKISRVDAASLKGLNNLAKLGLSFNSISAVDNGSLANTPHL 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LQELRAHENEITKVRKVTFNGLNQMIVIELGTNPLKSSGIENGAFQGMKKLSYIRIADTN
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                                                                                                                                                                                                                                                         Harper JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1388 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                      94US-0272919
                                                                                                                                                                                                                                                                                                                                                                                                   95WO-US08542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PG-40; proteoglycan; guanidinium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.8%;
                                                                                                                                                                                                                                                         Hernandez SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1709; DB 21;
Pred. No. 2.9e-144;
                                                                                      t decorin - using a strong anion interaction chromatography resi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                         Kostel
                                                                                                                                                                                                                                                         Pg,
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                                                                                                                                                                                                                                                           Parker
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                                                                                           and
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Disclosure; Fig 1A-D;

55pp; English.

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RESULT 8
AAR05160
ID AAR0
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human recombinant decorin (AAR89439) was obtd. by expression of a cDNA clone (AAT10741) in CHO host cells. Decorin (or PGII or PG-40) is a proteoglycan having a 40 kDa core protein. Recombinant decorin can be produced by cotransfection of CHO-DG44 cells with pSV2-decorin and pSV2dhfr. Large-scale cultures can be performed using CHO cells attached to microcarrier beads. The recombinant protein is purified from the cells using beads. The recombinant protein is purified from the cells using beads the recombinant protein is purified from the highly sensitive detection of guanidinium ions (ppm range), partic. In protein-contg. solns. purified using GuHC1, and also has therapeutic applns.
                                                                                                                                                                                                                                                                                                         25-MAR-2003
17-DEC-2001
09-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
WPI; 1990-178641/23.
N-PSDB; AAQ04491.
                                                                                                                                                                                                                                                   Osteoporosis; rheumatoid arthritis;
                                                                                                                                                                                                                                                                            Sequence of human bone proteoglycan II (decorin).
                                                                                                                                                                                                                                                                                                                                                                                         AAR05160 standard; protein;
                                           Termine
                                                                                                03-NOV-1989;
                                                                                                                          03-NOV-1989;
                                                                                                                                                     17-APR-1990.
                                                                                                                                                                               USN7432044-N
                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                      atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                 AAR05160;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EASGIGPEVPDDRDFEPSLGPVCPFRCQCHLRVVQCSDLGLDKVPKDLPPDTTLLDLQNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NPVQYWEIQPSTFRCVYVRSAIQLGNY 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LQELRAHENE I TKVRKVT FNGLNQM I VI ELGTNPLKSSGI ENGAFQGMKKLSY IRIADTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KITEIKDGDFKNLKNLHALILVNNKISKVSPGAFTPLVKLERLYLSKNQLKELPEKMPKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              NPVQYWEIQPSTFRCVYVRSAIQLGNY 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RELHLDNNKLTRVPGGLAEHKYIQVVYLHNNNISVVGSSDFCPPGHNTKKASYSGVSLFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RELHLDNNKLTRVPGGLAEHKYIQVVYLHNNNISVVGSSDFCPPGHNTKKASYSGVSLFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LQELRAHENEITKVRKVTFNGLNQMIVIELGTNPLKSSGIENGAFQGMKKLSYIRIADTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        342 AA;
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                                                                   INST OF
                                                                                                                                                                                                                                                                                                      (updated)
(updated)
(first entry)
                                                                                               89US-0142159
                                                                                                                          89US-0142159
                                                                                                                                                                                                                                     periodontal;
                                                                     HEALTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.5%; Score 1704; DB 17; 100.0%; Pred. No. 1.1e-144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                            353 AA
                                                                                                                                                                                                                                        human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                      Paget's disease;
bone matrix; pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>,</u>
                                                                                                                                                                                                                                     proteoglycan.
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Matches 319; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human bone matrix DNA and proteins - used in detection, diagnosis and treatment involving skeletal and/or connective tissue disease states.
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Pred. No. 4.3e-140;
2; Mismatches 7;
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09-JAN-2003
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maltose binding protein; tumour growth; inhibit
PG-40; transforming growth factor-beta; TGF-bet
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Pred. No. 7.4e-138;
0; Mismatches 0;
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DT 09-J7
DT 09-J7
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XX DE DECOI
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KW fueic
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Best Local Similarity
Matches 302; Conserv
                                                                                              25-MAR-2003
09-JAN-2003
28-APR-1994
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Ruoslahti EI;
                                                             Decorin sequence PT-77 (N-terminal
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(Updated on 25-MAR-2003 to
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Pred. No. 1.9e-132;
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leucine-rich repeat; proteoglycan; cell regulatory factor; MBP; fusion protein; maltose binding protein; tumour growth; inhibit decorin; PG-II; PG-40; transforming growth factor-beta; TGF-bet

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RESULT 12
AAR42265
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          Decorin sequence PT-76 (N-terminal
                                                                            AAR42265;
                                                                                                AAR42265 standard; Protein;
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on 25-MAR-2003 to
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                                  Biglycan; property pr
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                                                                                                                                               Rat neurotrophic biglycan
                                                                                                                                                                                                                         20-MAR-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ50051.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          on 09-JAN-2003 to add missing OS field.) on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LQELRAHENEITKVRKVTFNGLNQMIVIELGTNPLKSSGIENGAFQGMKKLSYIRIADTN 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KITEIKDGDFKNLKNLHALILVNNKISKVSPGAFTPLVKLERLYLSKNQLKELPEKMPKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KITEIKDGDFKNLKNLHALILVNNKISKVSPGAFTPLVKLERLYLSKNQLKELPEKMPKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EASGIGPEVPDDRDFEPSLGPVCPFRCQCHLRVVQCSDLGLDKVPKDLPPDTTLLDLQNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASGIGPEVPDDRDFEPSLGPVCPFRCQCHLRVVQCSDLGLDKVPKDLPPDTTLLDLQNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTSIPQGLPPSLTELHLDGNKISRVDAASLKGLNNLAKLGLSFNSISAVDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>LQELRAHENETTKVRKVTFNGLNQMIVIELGTNPLKSSGIENGAFQGMKKLSYIRIADTN</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ITSIPQGLPPSLTELHLDGNKISRVDAASLKGLNNLAKLGLSFNSISAVDN
                                  proteoglycan; chondroitin sulphate; neuron protection;
hic; central nervous system; CNS; memory loss; dementia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234 AĀ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craig W,
                                                                                                                                                                                                                     (first
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Pred. No. 2.4e-98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ğ,
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regulatory

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Best Local
                                                                                                                                                                                                                                                                                                                                                   Matches 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                    neurotrophic activity for brain neurons. Recombinant biglycan, obtd. by expression of encoding CDNA (ATOB9768) in eukaryotic host cells, can be used to enhance the survival and maintain the structure and function of CNS neurons during normal ageing as well as after pathological and/or traumatic nervous system damage. It can also be used to restore function following nervous system lesions and degenerative diseases, and to improve learning efficiency and memory in the elderly and in patients with dementia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proteoglycan cpds., partic. chondroitin sulphate proteoglycan(s) for maintain structural and function of the CNS and attenuating memory deficit(s) in the elderly and patients with dementia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-MAY-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
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                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rat biglycan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 44-45; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hasenoehrl R,
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                                                                                                                                                                                                                                                                                                                                                               Similarity
               FSNPVQYWEIQPSTFRCVYVRSAIQLGNYK 329
                                                                                   HLRELHLDNNKLTRVPGGLAEHKYIQVVYLHNNNISVVGSSDFCPPGHNTKKASYSGVSL 299
                                                                                                                                         TNITSIPQGLPPSLTELHLDGNKISRVDAASLKGLNNLAKLGLSFNSISAVDNGSLANTP 239
                                                        TLRELHLDNNKLSRVPAGLPDLKLLQVVYLHSNNITKVGINDFCPMGFGVKRAYYNGISL
                                                                                                                                                                                               KTLQELRAHENEITKVRKVTFNGLNQMIVIELGTNPLKSSGIENGAFQGMKKLSYIRIAD 179
                                                                                                                                                                                                                                                 FNNPVPYWEVQPATFRCVTDRLAIQFGNYK 368
                                                                                                              AKLTGIPKDLPETLNELHLDHNKIQAIELEDLLRYSKLYRLGLGHNQIRMIENGSLSFLP
                                                                                                                                                                        SSLVELRIHDNRIRKVPKGVFSGLRNMNCIEMGGNPLENSGFEPGAFDGL-KLNYLRISE
                                                                                                                                                                                                                                NNDISELRKDDFKGLQHLYALVLVNNKISKIHEKAFSPLRKLQKLYISKNHLVEIPPNLP
                                                                                                                                                                                                                                                                                        EASGSDTTSGVPDLDSLTPTFSAMCPFGCHCHLRVVQCSDLGLKTVPKEISPDTTLLDLQ
                                                                                                                                                                                                                                                                                                                   EASGIGPE---VPDDRDFEFSLGPVCPFRCQCHLRVVQCSDLGLDKVPXDLPPDTTLLDLQ
                                                                                                                                                                                                                                                                                                                                                                                                             369
                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AAR87951) is a chondroitin sulphate proteoglycan with activity for brain neurons. Recombinant biglycan, ression of encoding cDNA (AAT08768) in eukaryotic host
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Huston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Hypervariable_region
                                                                                                                                                                                                                                                                                                                                                              57.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Junghans
                                                                                                                                                                                                                                                                                                                                                51;
                                                                                                                                                                                                                                                                                                                                                              Score 985.5; DB 16;
Pred. No. 5.2e-80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        CC complexes (DAPCs) on the surface of a cell or activating a postsynaptic complexes (DAPCs) on the surface of a cell or activating a postsynaptic cc membrane of a cell that comprises contacting the cell with an effective amount of biglycan. A composition comprising biglycan or its portion cc is useful for treating or preventing a condition associated with abnormal CDAPC in cells, characterized by breakdown of muscle cell membrane, which circludes muscular dystrophies, such as Duchenne's, Becker's, Congenital, CC Limb-girdle muscular dystrophy and mytonic dystrophy and a condition cc characterized by abnormal neuromuscular junction or synapse, such as CC neuromuscular or neurological diseases in a subject. Neurological cc disorders, include polymyositis and Alzheimer's disease. Biglycan is also CC useful for preventing and treating smooth muscle disorders, such as CC cardiac myopathies and for treating and inhibiting infections of cells by CC microorganisms e.g. viruses. Agents that modulate the activity of CC DAG-125, identified by the methods are useful in the prophylactic and CC unstable DAPC or an inappropriate formation of a postsynaptic cunstable DAPC or an inappropriate formation of a postsynaptic of constable cell or tissue culture and, tissues can be incubated in vitro CC with biglycan to reverse tissue atrophy and to improve their growth or constable coll in vitro. The present sequence represents the human biglycan.
                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB85043;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stabilizing dystrophin-associated protein complexes and activating postsynaptic membrane of a cell for treating or preventing muscular, neuromuscular and neurological disorders, involves contacting cell with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-355617/37.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fallon J, McKechnie B,
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                                                                                                                                                                                                                                                               189;
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NDISELRKDDFKGLQHLYALVLVNNKISKIHEKAFSPLRKLQKLYISKNHLVEIPPNLPS
                                     NKITEIKDGDFKMLKNLHALILVNNKISKVSFGAFTPLVKLERLYLSKNQLKELFEKMFK 120
                                                                                                                                                                 EASGIGPE-VPDDRDFEPSLGPVCPFRCQCHLRVVQCSDLGLDKVPKDLPPDTTLLDLQN
                                                                                                                               EASGADTSGVLDPDSVTPTYSAMCPFGCHCHLRVVQCSDLGLKSVPKEISPDTTLLDLQN
                                                                                                                                                                                                                                                                                                                                                                                            368 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rafii M,
                                                                                                                                                                                                                                                     50,;
                                                                                                                                                                                                                                                            Score 979; DB 2
Pred. No. 2e-79;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Creely H,
                                                                                                                                                                                                                                                                                                                     22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bowe
                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                     Indels 2;
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                                               The invention relates to stabilizing collagen VI-dependent dystrophin-
associated protein complexes (DAPCs) on the surface of a cell. The
method involves contacting the cell with biglycan therapeutic. The method
is useful for preparing a composition for treating neuromuscular or
neurological disease. The present sequence represents a human biglycan
                                                                                                                                                                                                                                                                     Stabilizing collagen VI-dependent dystrophin-associated protein complexes on the surface of a cell for preparing a composition for treating neuromuscular or neurological disease by contacting the cell with biglycan therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
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                                                                                                                                                                                                                   Claim 8;
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27-JUN-2001;
18-JUL-2001;
25-SEP-2001;
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Monahan JE,
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                                                                            Breast cancer diagnosis expression of a marker i
                                                             non-breast cancer sample
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DB; ACC50090.
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; 2001US-301572P.
; 2001US-30501P.
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Sahin A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                is afflicted with breast cancer. The method comprises comparing the level of expression of a marker (gene/polypeptide see ACC50076 to ACC50334 and ABR47386 to ABR47632) in a patient sample and the normal level of expression of the marker in a control non-breast cancer sample, where a significant increase in the level of expression of the marker in the patient is an indication that the patient is afflicted with breast cancer. The breast cancer associated sequences from the present invention have cytostatic activities and can be used in gene therapy. The method is useful for diagnosing and treating breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N.B. The sequence data for this patent did not specification, but was obtained in electronic f at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a method for assessing whether a patient is afflicted with breast cancer. The method comprises comparing the level of expression of a marker (come/nolumentia)
                       Christgau
                                                                          23-MAY-2001;
                                                                                                 22-MAY-2002; 2002WO-EP05612
                                                                                                                              28-NOV-2002
                                                                                                                                                       WO200295415-A2
                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                          Human;
                                                                                                                                                                                                                                 Human biglycan protein.
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                       PAC;
                                                                                                                                                                                                       arthritis; biglycan
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/label= Sig\_peptide

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16-NOV-1995 WO9530432-A1.

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RESULT 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biglycan; property pr
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Pred. No. 2e-79;
0; Mismatches
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RESULT 19
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Best Local S
Matches 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human biglycan (AAR87952) is a chondroitin sulphate proteoglycan wit neurotrophic activity for brain neurons. It can be used to enhance the survival and maintain the structure and function of CNS neurons during normal ageing as well as after pathological and/or traumatic nervous system damage. It can also be used to restore function following nervous system lesions and degenerative diseases, and to improve learning efficiency and memory in the elderly and in patient with armore.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proteoglycan cpds., partic. chondroitin sulphate proteoglycan(s) for maintain structural and function of the CNS and attenuating memory deficit(s) in the elderly and patients with dementia
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Mueller HW;
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            Bos taurus
                                           neurotrophic;
                                                       Biglycan;
                                                                          Bovine neurotrophic biglycan
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Similarity 57.3%;
89; Conservative 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                       EASGIGPE--VPDDRDFEPSLGPVCPFRCQCHLRVVQCSDLGLDXVPKDLPPDTTLLDLQ
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                                                                                                                                                                                                                                                                                                                                                                                NNDISELRKDDFKGLQHLYALVLVNNKISKIHEKAFSPLRKLQKLYISKNHLVEIPPNLP
                                                                                                                                                                                                                                                                                                                                                                                                                            EASGADTTSGVLDPDSVTPTYSAMCPFGCHCHLRVVQCSDLGLKSVPKEISPDTTLLDLQ
                                                                                                                                                                                                                                                        HLRELHLDNNKLTRVPGGLAEHKYIQVVYLHNNNISVVGSSDFCPPGHNTKKASYSGVSL 299
                                                                                                                                                                                                                                                                                                                TNITSIPQGLPPSLTELHLDGNKISRVDAASLKGLNNLAKLGLSFNSISAVDNGSLANTP 239
                                                                                                                                             standard;
                                                                                                                                                                                                                                                                                         AKLTGIPKDLPETLNELHLDHNKIQAIELEDLLRYSKLYRLGLGHNQIRMIENGSLSFLP
                                                                                                                                                                                                   FNNPVPYWEVQPATFRCVTDRLAIQFGNYK 368
                                                                                                                                                                                                                      FSNPVQYWEIQPSTFRCVYVRSAIQLGNYK 329
                                                                                                                                                                                                                                              TLRELHLDNNKLSRVPAGLPDLKLLQVVYLHSNNITKVGVNDFCPMGFGVKRAYYNGISL
                                           proteoglycan; chondroitin sulphate; neuron protection;
nic; central nervous system; CNS; memory loss; dementia
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Pred. No. 2.2e-79;
51; Mismatches 87;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-NOV-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KTLQELRAHENEITKVRKVTFNGLNQMIVIELGTNPLKSSGIENGAFQGMKXLSYIRIAD 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TLRELHLDNNKLSRVPAGLPDLKLLQVVYLHTNNITKVGVNDFCPVGFGVKRAYYNGISL
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Pred. No. 2.9e-79;
1; Mismatches 87;
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biglycan

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                                                                                                                                                                                                                                                                        The invention relates to the inhibition of transforming growth CC factor-beta (TGF-beta) activity involving contacting TGF-beta with a CC purified polypeptide comprising leucine-rich amino acid sequence of a CC member of decorin superfamily of mammalian proteoglycans. The following activities can be attributed to the polypeptide of the invention:
CC cytostatic, nephrotropic, antirheumatic, antiarthritic, vasotropic, antiarteriosclerotic, hepatotropic, cardiant, dermatological and CC vulnerary. Polypeptides of the invention act as transforming growth factor-beta (TGF-beta) binder. The polypeptides of the invention can be CC disease by a transforming growth factor-beta (TGF-beta) binder. The polypeptides of the invention can be CC caused by a transforming growth factor-beta (TGF-beta) regulated CC disease, glomerulonephritis, rheumatoid arthritis, arteriosclerosis, adult respiratory distress syndrome, cirrhosis of liver, fibrosis of lungs, post-myocardial infarction, cardiac fibrosis, post-angioplasty conditions such as keloids and scarring resulting from burn injuries; other investive skin injuries and reconstructive surgery. The wounds CC conditions such as keloids and scarring resulting from burn injuries; other investive skin injuries and reconstructive surgery. The wounds CC reated with the polypeptide, particularly decorin exhibit no detectable scarring, and are histologically normal. The current sequence represents
                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                        Sequence
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13-MAY-1992;
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17-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adult respiratory distress syndrome; Cirrhosis; Cancer; Fibrotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nephrotropic; Antirheumatic; Antiarthritic; Vasotropic; Vulnerary Antiarteriosclerotic; Hepatotropic; Cardiant; Dermatological; Glomerulonephritis; Rheumatoid arthritis; Arteriosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fibromodulin; Decorin; Biglycan; Proteoglycan; Extracellular matrix; TGF-beta; Transforming growth factor-beta; Burn; Wound; Cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BURN-) BURNHAM INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-JUN-1988
                                                                                                                                                                                                                  Local
                      121
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                                                                                         61
                                                                                                                                                                                                 186;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        decorin or biglycan polypeptide for inhibiting treatment of dermal wounds and cancer -
                                                                                                                                                              N
                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; Fig 11; 40pp;
TLQELRAHENEITKVRKVTFNGLNQMIVIELGTNPLKSSGIENGAFQGMKKLSYIRIADT
                                                                                  NKITEIKOGDFKNLKNLHALILVNNKISKVSPGAFTPLVKLERLYLSKNQLKELPEKMPK
                                                      NDISELRKDDFKGLQHLYALVLVNNKISKIHEKAFSPLRNVQKLYISKNHLVEIPPNLPS
                                                                                                                         EASGADTSGVLDPDSVTPTYSAMCPFGCHCHLRVVQCSDLGLKSVPKEISPDTTLLDLQN
                                                                                                                                             EASGIGPE-VEDDRDFEPSLGPVCPFRCQCHLRVVQCSDLGLDKVFKDLFPDTTTLDLQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EI,
                                                                                                                                                                                                                                                                       368
                                                                                                                                                                                                 Conservative
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94US-0303238.
88US-0212702.
90US-0467888.
92US-0882345.
                                                                                                                                                                                                                                                                       AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91US-0792192.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95US-0458834.
                                                                                                                                                                                            56.4%; Score 966; DB 22; 56.5%; Pred. No. 2.9e-78; tive 51; Mismatches 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English.
                                                                                                                                                                                                                                 Length 368;
                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGF-beta activity
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                                                                                                                                                                                              Gaps
                  180
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Conservative

53;

Indels

2

Gaps

60

EASGIGPE-VPDDRDFEPSLGPVCPFRCQCHLRVVQCSDLGLDXVPXDLPPDTTLLDLQN

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ARBSULT 21
AAROS159
ID AAROS5
XX AAROS
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XX AAROS
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XX AROS
XX AROS
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Query Match
Best Local Similarity
Matches 185; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAR-2003
17-DEC-2001
09-OCT-1990
                                                                                                                                                           Probes and Abs raised to the proteins can be used to determine their levels useful in diagnosis of associated conective tissue diseases states such as osteoporosis, osteo/rheumatoid arthritis, paget's disease, artherosclerosis and periodontal disease. Proteins may also be used to induce or block biological function. (Note: Revised entry submitted to correct the patent number format of US Government-owned NTIS applications to prevent clashes with ongoing US granted patent numbers. For further information please visit the Derwent web site at www.derwent.com/dwpi/updates/ntis_us.html.) (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Osteoporosis; rhe atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human bone matrix DNA and proteins - used in detection, diagnosis and treatment involving and/or connective tissue disease states.
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                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page ?; ?pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-NOV-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence of human bone proteoglycan I (biglycan).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LRELHLDNNKLTRVPGGLAEHKYIQVVYLHNNNISVVGSSDFCPPGHVTKKASYSGVSLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NNPVPYWEVQPATFRCVTDRLAIQFGNYK 367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KUTGIPKDLPETLNELHLDHNKIQAIELEDLLRYSKLYRLGLGHNQIRMIENGSLSFLPT
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(updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rheumatoid arthritis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89US-0142159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     periodontal; human
                          56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English
Score 965; DB 11;
Pred. No. 3.6e-78;
3; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
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bone matrix; proteoglycan.
                                                    Length 368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   skeletal
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RESULT 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                          leucine-rich repeat; proteoglycan; cell regulatory factor; MBP; fusion protein; maltose binding protein; tumour growth; inhibitio decorin; PG-II; PG-40; transforming growth factor-beta; TGF-beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Decorin sequence PT-75 (N-terminal to LRR6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAR-2003
09-JAN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR42264
                                             Active fragments of decorin (full-length coding sequence AAQ50046) were generated by PCR and fused to Maltose Binding Protein. The resulting fusion proteins were useful for inhibiting the activity of a cell regulatory factor, esp. TGF-beta, and hence for treating conditions associated with over-activity of the growth factor such as certain tumours.
                                                                                                                                                                                                                                                     Cardenas J,
Ruoslahti EI;
                                                                                                                                                                                                                                                                                                                                          02-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                            WO9320202-A1
                                                                                                                                                                                                                N-PSDB;
                                                                                                                                       Claim 10; Page 43-44; 77pp; English.
                                                                                                                                                                         Active fragments of protein esp. decorin - with cell regulatory factor domain, useful for inhibiting cell regulatory factor
                                                                                                                                                                                                                                                                                                                  03-APR-1992;
Sequence
                        (Updated
(Updated
                                                                                                                                                                                                                                                                                        (LJOL-) LA JOLLA CANCER RES FOUND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NKITEIKOGDFKNLKNLHALILVNNKISKVSPGAFTPLVKLERLYLSKNOLKELPEKMPK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNPVQYWEIQPSTFRCVYVRSAIQLGNYK 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LRELHLDNNKLTRVPGGLAEHKYIQVVYLHNNNISVVGSSDFCPPGHNTKKASYSGVSLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLTGIPKDLPETLNELHLDHNKIQAIELEDLLRYSKLYRLGLGHNQIRMIENGSLSFLPT 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NDISELRKDDFKGLQHLYALVLVNNKISKIHEKAFSPLRNVQKLYISKNHLVEIPPNLPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NNPVPYWEVOPATERCVTDRLAIQFGNYK 367
                       on 09-JAN-2003 to add missing OS field.) on 25-MAR-2003 to correct PN field.)
 186 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (updated)
(updated)
(first entry)
                                                                                                                                                                                                                                                               Craig W,
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                                                                                                                                                                                                                                                                                                                                           93WO-US03171
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                                                                                                                                                                                                                                                                 Mullen DG,
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                                                                                                                                                                                                                                                                  Pierschbacher
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RESULT 23
AABO1311
ID AABO1311
AC AABO1311
AC AABO1311
AC AABO13X
AC AABO1
AC PRO;
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Best Local Similarity
Matches 183; Conserv
                                                               01-DEC-1998;
16-DEC-1998;
22-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRO; membrane bound protein; secreted protein; PRO357; PRO327; PRO243; PRO715; PRO241; PRO323; PRO299; PRO233; PRO344; PRO347; PRO355; PRO353; PRO361; PRO365; transmembrane polypeptide; antibody; screening; detection; inhibition; probe; primer; human.
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                                                               98WO-US25108.
98US-0112850.
98US-0113296.
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282..288
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237..243
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Pred. No. 4.5e-77
0; Mismatches 0
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ID AAU12
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Best Local S
Matches 175
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Gerritsen I
Hillan KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human nucleic acids encoding secreted and transmembrane polypeptides which are designated as PRO polypeptides are described The membrane-bound proteins have various industrial applications, including as pharmaceutical and diagnostic agents. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. Anti-PRO antibodies are useful for the affinity purification of PRO from recombinant cell culture or natural sources.
                           WO200140466-A2
                                                                          breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal mu adipocyte; A-peptide; factor VIIA; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
                                                                                                                                                 Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 12;
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                                                                                                                                                                                                                                 AAU12335 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
                                                                                                                     secretory and transmembrane;
                                                                                                                                                PRO241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FKNLKNLHALILVNNKISKVSPGAFTPLVKLERLYLSKNQLKELPEKMPKTLQELRAHEN 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRSHFFFFDLFFMCFFGCQCYSRVVHCSDLGLTSVPTNIFFDTRMLDLQNNKIKEIKEND
                                                                                                                                                                                                                                                                                                                                                                                                                                       PSLTELHLDGNKISRVDAASLKGLNNLAKLGLSFNSISAVDNGSLANTPHLRELHLDNNK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHEN
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des, designated
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                                                                                                                                                polypeptide sequence
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A, Godowski PJ, Grimaldi CJ, Gurn
Napier MA, Roy MA, Tumas D, Woo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English
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Pred. No. 3.2e-
60; Mismatches
                                                                                                                                                                                                                                                                                                    377
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                                                                                                                  PRO; mammalian; cancer; lung;
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                                                                                         muscle;
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CC PRO polypeptides, and to detect the presence of mammalian lung, colon, cc breast, prostate, rectal, cervical or liver tumours by comparing PRO cc polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, the cc proliferation or differentiation of chondrocytes, the proliferation or cartilage, the proliferation of inner ear utricular supporting cells or cof T-lymphocytes, the release of a cytokine from peripheral blood comoncytes (PBNCs), or the proliferation of endothabital cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide co factor VIIA. The PRO polypeptides can be used in assays to identify colourer idea can be insed to concerns a polymentides encoding colourer idea can be insed to concerns a polymentides 
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PRO polypeptides, 1
PRO polypeptides, t
PRO polypeptides, t
PRO polypeptides, a
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Smith V,
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20-MAR-2000;
21-MAR-2000;
30-MAR-2000;
17-MAY-2000;
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06-JAN-2000;
11-FEB-2000;
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02-DEC-1999;
09-DEC-1999;
16-DEC-1999;
20-DEC-1999;
20-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 12; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g. lung, breast, prostate, cervical -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
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18-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-DEC
                               PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy.
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DB; AAS21407.
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1 ME, Goddard
Stewart TA,
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2000WO-US04314.

2000WO-US04914.

2000WO-US05004.

2000WO-US05001.

2000WO-US05601.

2000WO-US07377.

2000WO-US07379.

2000WO-US08439.

2000WO-US13705.

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2000WO-US00376.
2000WO-US03565.
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99WO-US30095.
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                                                                                                                                                                                                                                                                                                                                                                      represent novel human secretory and transmembrane The PRO polypeptides are useful to detect or the transmembrane
                                                                                                                                                                                                                                                                                                                                The PRO polypeptides are useful to detect other to link bioactive molecules to cells expressing to modulate biological activities of cells expressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     I A, Gc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Deforge L, Desnoyers L, Filva
A, Godowski PJ, Gurney AL, Sh
Tumas D, Watanabe CK, Wood WI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Filvaroff E, G
L, Sherwood S;
od WI, Zhang Z;
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Query Match Best Local Sin Matches 175;

Similarity

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Score 943.5; Pred. No. 3.2 Mismatches

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29-JUL-2000;
25-JUL-2000;
25-JUL-2000;
26-JUL-2000;
20-AUG-2000;
17-AUG-2000;
23-AUG-2000;
23-AUG-2000;
24-AUG-2000;
07-SEP-2000;
07-SEP-2000;
18-SEP-2000;
18-SEP-2000;
18-NOV-2000;
24-DOV-2000;
20-DEC-2000;
20-DE
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   2000US-24292P
2000US-070938
2000WO-US30952
2000WO-US38678
2000WO-US38678
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2000US-0767609
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22-MAR-2001;
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10-MAY-2001;
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25-MAY-2001;
25-MAY-2001;
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01-JUN-2001;
20-JUN-2001;
28-JUN-2001;
                                                                                                                                                                                                                             The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The present sequence is a PRO protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Baker KP, Ferrara N,
Godowski PJ, Gurney A
Stephan JF, Watanabe
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(GERR/)
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(BAKE/)
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                                                                                                                                                                                                                                                                                                                                   Claim 11; Fig
                                                                                                                                                                                                                                                                                                                                                     One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal -
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GODOWSKI P J.
GURNEY A L.
HILLAN K J.
MARKTERS S A.
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PAONI N F.
STEPHAN J F.
WATANABE C K.
WILLIAMS P M.
WOOD W I.
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BAKER K P.
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PSLTELHLDGNKISRVDAASIKGLNNLAKIGLSENSISAVDNGSLANTPHLRELHLDNNK
                                  EITKVRKVTFNGLNOMIVIELGTNPLKSSGIENGAFQGMKKLSVIRIADTNITSIPQGLP
                                                                          FKNLKNILHALIILVNNKISKVSPGAFTPLVKLERLYLSKNQLKELPEKMPKTLQELRAHEN
                                                                                                                        PRSHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKEND
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2001US-0816744

2001US-0828366

2001US-0854208

2001US-0854280

2001US-0856034

2001US-0866034

2001US-0870574

2001WS-0870574

2001WG-US17800

2001WG-US17800
                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               Gurney AL, F
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                                                                                                                                                                                                                                                                                                                                   30; 567pp; English.
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L, Hillan KJ, Marsters SA,
CK, Williams PM, Wood WI,
                                                                                                                                                                   60;
                                                                                                                                                                             Score 943.5; DB 2
Pred. No. 3.2e-76;
                                                                                                                                                                     Mismatches
                                                                                                                                                                     82;
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3A, Pan J,
[, Ye W;
                                                                                                                                                                     Indels
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    18-SEP-2000
24-OCT-2000
24-OCT-2000
08-NOV-2000
08-NOV-2000
01-DEC-2000
20-DEC-2000
20-DEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-AUG-2000;
07-SEP-2000;
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20-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LTRVPGGLAEHKYIQVVYLHNNNISVVGSSDFCPPGHNTKKASYSGVSLFSNPVQYWEIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PATERCVLSRMSVQLGNF 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNK
                                                             2001US-0828366.
2001US-0854208.
2001US-0854280.
2001US-0866028.
2001US-0866034.
2001WO-US17092.
                                                                                                                                                                                   2001WO-US06666.
2001US-0802706.
2001US-0808689.
2001US-0816744.
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2001WO-US06520
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2000WO-US34956
                                                                                                                                                                                                                                                                                                                                                                        2000WO-US30873
2000WO-US32678
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2000US-230978P
                         2001US-0870574
2001WO-US17443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000WO-US20710
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mapping; gene mapping.
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RESULT 27
ABU66733
ID ABU66
XX
ABU66
XX
AC ABU66
XX
DT 23-M2
XX
DT 23-M2
XX
Humar
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Human PRO F Human; PRO

polypeptide;

secreted and transmembrane

protein;

PRO polypeptide #164.

АВU66733; 23-мау-2003

(first entry)

ABU66733 standard;

Protein;

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Best Local S
Matches 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic activities, and can be used in gene therapy. The PRO polynucleotides, proteins, agonists and antagonists are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restensosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophiabitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO polynucleotides have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. ABL88259 to ABL88267 represent primers and probes used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               One hundred and eighty seven nucleic acids encoding PRO polynuseful in diagnosis and treatment of cardiovascular (e.g. myinfarction), endothelial or angiogenic disorders in a mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-090516/12.
N-PSDB; ABL88086.
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Stephan JF, Watanabe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABL88072 to ABL882
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH
360
                              311
                                                                                                                            240
                                                                300
                                                                                            251 LTRVPGGLAEHKYIQVVYLHNNNISVVGSSDFCPPGHNTKKASYSGVSLFSNPVQYWEIQ
                                                                                                                                                            191
                                                                                                                                                                                           181 KVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIAEAKLTSVPKGLP
                                                                                                                                                                                                                         131 EITKVRKVTFNGLNQMIVIELGTNPLKSSGIENGAFQGMKKLSYIRIADTNITSIPQGLP
                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                           175;
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                                                                                                                                                                                                                                                                                                                                                           1
                                                                                                                                                                                                                                                                                                                           61 PRSHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKEND
                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
PATERCYLSRMSVQLGNF
                              PSTFRCVYVRSAIQLGNY 328
                                                            LKKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQ
                                                                                                                           PTILELHLDYNKISTVELEDFKRYKELORLGLGNNKITDIENGSLANIPRVREIHLENNK
                                                                                                                                                  PSLTELHLDGNKISRVDAASLKGLNNLAKLGLSFNSISAVDNGSLANTPHLRELHLDNNK
                                                                                                                                                                                                                                                         FKGLTSLYGLILMNNKLTKIHPKAFLTTKKLRRLYLSHNOLSEIPLNLPKSLAELRIHEN
                                                                                                                                                                                                                                                                             FKNLKNLHALILVNNKISKVSPGAFTPLVKLERLYLSKNQLKELPEKMPKTLQELRAHEN
                                                                                                                                                                                                                                                                                                                                             PDDRDFEPSLGPVCPFRCQCHLRVVQCSDLGLDKVPKDLPPDTTLLDLQNNKITEIKDGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                        379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABL88258 encode the PRO proteins given in ABB84817 he PRO proteins and polynucleotides have cardiant, conic, hypotensive, vulnerary and antiarteriosclerotic
                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INC
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L, Hillan KJ, Ma
CK, Williams PM,
                                                                                                                                                                                                                                                                                                                                                                                        60;
                                                                                                                                                                                                                                                                                                                                                                                        Score 943.5;
Pred. No. 3.2e
60; Mismatches
377
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                                                                                                                                                                                                                                                                                                                                                                                                        943.5; DB 2
No. 3.2e-76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wood WI, Ye
                                                                                                                                                                                                                                                                                                                                                                                         82;
                                                                                                                                                                                                                                                                                                                                                                                                                        23;
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Ye W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRO polypeptides, (e.g. myocardial
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                                                                                                                                                                                                                                                                                                                                                                                                                        379;
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                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
differentiation; chondrocyte; tumour; genetic disorder;
cytostatic.
   2000WO-US04414
2000WO-US05004
2000WO-US05004
2000WO-US05601
2000WO-US05841
2000WO-US05841
2000WO-US06319
2000WO-US06884
2000WO-US07377
2000WO-US07532
2000WO-US07532
2000WO-US13705
2000WO-US13705
2000WO-US14941
                                                                                                                                                                                                                                       99WO-US28565.
99WO-US30915.
99WO-US30919.
99WO-US30999.
99WO-US31274.
99WO-US31274.
2000WO-US00277.
2000WO-US00277.
2000WO-US00277.
2000WO-US00376.
2000WO-US03365.
2000WO-US04341.
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99WO-US20594.
99WO-US21090.
99WO-US21547.
99WO-US21308.
99WO-US28214.
99WO-US28213.
99WO-US28313.
99WO-US28313.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US28634.
99WO-US28551.
99WO-US28564.
        The present invention relates to the isolation of novel human PRO CC polypeptides, and the polymucleotide sequences encoding them. The CR polypeptides are secreted and transmembrane proteins. The PRO CC polypeptides are useful for detecting other PRO polypeptides, for CC linking bioactive molecules to cells expressing PRO polypeptides, for CC for modulating biological activities of cells expressing PRO polypeptides, core polypeptides, and for for identifying agonists or antagonists. CC the PRO polypeptides are useful for for stimulating the release of tumour necrosis factor (TNF)-alpha from human blood, for stimulating the proliferation or differentiation of chondrocytes, and detecting the presence of tumours. The polymucleotide sequences encoding PRO CC polypeptides are useful as hybridisation probes, in chromosome and CC gene mapping, in the generation of antisense RNA and DNA, in the greence of the prolypeptides, for generating transgenic animals or CC knockout animals, for the genetic analysis of individuals with genetic disorders, and in gene therapy. ABU66570-ABU66844 represent the human CR PRO polypeptides of the invention.

CC comparation of the propertion of the sequence data for this patent was obtained in electronic comparation for the USPRO web site at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-JUN-2000; 2000WO-US15264.
28-JUL-2000; 2000WO-US20371.
11-AUG-2000; 2000WO-US23322.
24-AUG-2000; 2000WO-US233328.
08-NOV-2000; 2000WO-US33952.
10-NOV-2000; 2000WO-US33953.
20-DEC-2000; 2000WO-US34956.
28-FEB-2001; 2001WO-US36520.
01-MAR-2001; 2001WO-US17090.
01-JUN-2001; 2001WO-US17090.
02-JUN-2001; 2001WO-US20116.
29-JUN-2001; 2001WO-US20116.
29-JUN-2001; 2001WO-US20116.
29-JUN-2001; 2001WO-US21735.
20-DEC-2000; 2001WO-US21735.
20-DEC-2000; 2001WO-US21735.
20-DEC-2000; 2001WO-US21735.
20-DEC-2000; 2001WO-US21735.
20-DEC-2000; 2001WS-0806608.
14-MAR-2001; 2001US-0806608.
10-MAY-2001; 2001US-0854208.
11-MAY-2001; 2001US-0854208.
11-MAY-2001; 2001US-0866034.
25-MAY-2001; 2001US-0866034.
01-JUN-2001; 2001US-0866342.
21-JUN-2001; 2001US-0886342.
21-JUN-2001; 2001US-0886342.
21-JUN-2001; 2001US-0887879.
18-JUL-2001; 2001US-0898877.
06-AUG-2001; 2001US-0931836.
119-DEC-2001; 2001US-0931836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Baker KP, Beresini M,
Gerritsen ME, Goddard
Smith V, Stewart TA,
                                                                                                                                                                                                                                                                                                                                                                               New secreted and transmembrane PRO nucleic acids, useful for gene therapy, in chromosome and gene mapping, as chromosome markers, in tissue typing, and in chromosome identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-332040/31.
N-PSDB; ACA03766.
                                                                                                                                                                                                                                                                                                                                                 Claim 12; Fig 328; 660pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DeForge L, Desnoyers L,
, Godowski PJ, Gurney
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          y AL, Sherwood S; Wood WI, Zhang Z;
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L, Sherwood S;
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29-OCT-1998; 29-OCT-1998; 20-NOV-1998; 01-DEC-1998; 05-JAN-1999;

-0M66 -0M86 -0M86 -0M86 -0M86

-US24855

99WO-US05028. 99WO-US05190. 99WO-US08615.

-US00106

99WO-US10733. 99WO-US12252.

14-SEP-1998; 16-SEP-1998; 17-SEP-1998; 07-OCT-1998;

-0M86

-US19330 -US19094 LO-SEP-1998

0M86 0M86 0M86

-US18824

20-FEB-2003 US2003036180-A1 Homo sapiens.

2002US-0143114.

97WO-US05230 98WO-US12456

08-MAR-1999
10-APR-1999
20-APR-1999
11-SEP-1999
01-SEP-1999
11-SEP-1999
11-SEP-1999
11-SEP-1999
11-SEP-1999
11-SEP-1999
11-SEP-1999
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30-NOV-1999
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02-DEC-1999
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02-DEC-1999
02-DEC-1999
02-DEC-1999
03-DEC-1999
03-DEC-1999
03-DEC-1999
03-DEC-1999
03-DEC-1999
04-FEB-2000
06-JAN-2000
01-FEB-2000
01-FEB-2000
01-WAR-2000

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RESULT 28
ABU67009
ID ABU677
XX
XX ABU677
AC ABU677
AC ABU677
XX
DT 27-MA
XX infel
XX infel
XX infel
XX infel
XX biore
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         31-MAR-1997
12-JUN-1998
14-JUL-1998
28-AUG-1998
10-SEP-1998
14-SEP-1998
14-SEP-1998
14-SEP-1998
17-SEP-1998
16-SEP-1998
07-OCT-1998
29-OCT-1998
29-OCT-1998
29-OCT-1998
29-OCT-1998
30-DEC-1998
01-DEC-1998
05-JAN 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; secreted protein; transmembrane protein; PRO; inflammatory disease; organ failure; atherosclerosis; cardiac injury; infertility; birth defects; premature aging; AIDS; biosensor; acquired immunodeficiency syndrome; cancer; diabetic complication; bioreactor; tumour.
                                                                                                                                                                                                                                                                                                            03-MAY-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human secreted/transmembrane,
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         97WO-US05230

98WO-US14552

98WO-US148552

98WO-US18824

98WO-US19824

98WO-US1993

98WO-US1993

98WO-US19437

98WO-US21141

98WO-US21141

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ismatches 82;
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     17-MAR-2000
17-MAY-2000
22-MAY-2000
30-MAY-2000
30-MAY-2000
23-AUG-2000
24-AUG-2000
24-AUG-2000
24-AUG-2000
20-DEC-2000
20-DEC
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22-FEB-2000;
24-FEB-2000;
24-FEB-2000;
01-MAR-2000;
02-MAR-2000;
02-MAR-2000;
110-MAR-2000;
15-MAR-2000;
21-MAR-2000;
21-MAR-2000;
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20-DEC-1999
22-DEC-1999
30-DEC-1999
30-DEC-1999
30-DEC-1999
05-JAN-2000
06-JAN-2000
06-JAN-2000
11-FEB-2000
11-FEB-2000
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01-DEC-1999;
01-DEC-1999;
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02-DEC-1999;
02-DEC-1999;
16-DEC-1999;
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15-SEP-1999;
05-OCT-1999;
29-NOV-1999;
30-NOV-1999;
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02-JUN-1999;
01-SEP-1999;
08-SEP-1999;
13-SEP-1999;
15-SEP-1999;
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20-APR-1999;
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2000WO-US14042
2000WO-US14941
2000WO-US15264
2000WO-US27710
2000WO-US23522
2000WO-US23328
2000WO-US23328
2000WO-US33673
2000WO-US33673
2000WO-US32678
2001WO-US36666
2001WO-US17092
2001WO-US17092
2001WO-US17092
2001WO-US17092
2001WO-US27136
2001WO-US27136
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2001US-0806869
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2001US-0866218
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2000WO-US03565.
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2000WO-US05746.
2000WO-US05841.
2000WO-US06319.
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2000WO-US07377.
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2000WO-US05004.
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2000WO-US13705
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99WO-US21940
99WO-US211947
99WO-US21547
99WO-US28214.
99WO-US28313
99WO-US28313
99WO-US28301.
99WO-US28551.
99WO-US28551.
99WO-US28556.
99WO-US2856.
99WO-US30095.
99WO-US30095.
99WO-US30095.
99WO-US310720.
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99WO-US05190.
99WO-US08615.
99WO-US10733.
99WO-US12252.
99WO-US20111.
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The invention relates to an isolated nucleic acid comprising, or which is cat least 80% identical to, or the full-length coding sequence of, any of the 275 nucleotide sequences, encoding the corresponding PRO polypeptide come of 275 secreted or transmembrane proteins). The nucleic acid come of 275 secreted or transmembrane proteins. The nucleic acid come of 275 secreted or transmembrane proteins. The nucleic acid come of 275 secreted or transmembrane proteins. The nucleic acid come of 275 secreted or transmembrane proteins. The nucleic acid come of 275 secreted or transmembrane proteins. The nucleic acid come of 275 secreted or the DNA deposited come of the calls of the proliferation of the proliferation of the proliferation of the calls, the release of the proliferation of the proliferation of the calls, the release of the proliferation of the proliferation of the calls, the release of the proliferation of the proliferation of the calls, the release of the proliferation of the properties of the proliferation of the properties of the uptake of glucose or free fatty acid (FFA) by skeletal muscle cells, the release come of the defect of the nucleotide sequences of the defect of the proliferation of adipocyte cells, a method for detecting the uptake of the defect of the proliferations. The nucleic and and an oligonucleotide probe derived the probe derived the probe derived the probe derived the proliferations. The nucleic acids are useful as hybridisation or the proliferation of the proliferation of the proliferation or bioreactors. Both are useful in tissue typing.

The present sequence represents a PRO protein of the invention.
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Best Local
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05-JUN-2001; 2001US-0874503.
14-JUN-2001; 2001US-0882636.
19-JUN-2001; 2001US-0886342.
21-JUN-2001; 2001US-0887879.
18-JUL-2001; 2001US-0908827.
06-AUG-2001; 2001US-0924419.
09-AUG-2001; 2001US-0927796.
16-AUG-2001; 2001US-0931836.
19-DEC-2001; 2001US-0038072.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New secreted and transmembrane nucleic acids and polypeptides, designated as PRO, useful for treating inflammation, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, or cancer
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Gerritsen ME, Goddard
                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                 Similarity
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                                                                                                                           PRSHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKEND
                                                                                                                                                                  PDDRDFEPSIGPVCPFRCQCHLRVVQCSDLGLDKVPKDLPPDTTLLDLQNNKITEIKDGD
EITKVRKVTFNGLNQMIVIELGTNPLKSSGIENGAFQGMKKLSYIRIADTNITSIPQGLP 190
                                         FKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHEN
                                                                     FKNLKNIHALILVNNKISKVSPGAFTPLVKLERLYLSKNQLKELPEKMPKTLQELRAHEN 130
                                                                                                                                                                                                                                                                                              379
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A, Godowski PJ, Gurney AL,
                                                                                                                                                                                                              60;
                                                                                                                                                                                                                             Score 943.5;
Pred. No. 3.2
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                                                                                                                                                                                                                               .2e-76;
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L, Sherwood S;
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                                                                                                                                                                                                                                                   Length 379;
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01-DEC-2000;
28-FEB-2001;
03-DEC-1997;
11-DEC-1997;
11-DEC-1997;
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12-DEC-1997;
16-DEC-1997;
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15-SEP-1999;
30-NOV-1999;
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02-MAR-2000;
30-MAR-2000;
22-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABU67121 standard; Protein;
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2000WO-US04414.
2000WO-US05841.
2000WO-US08439.
2000WO-US14042.
2000WO-US14042.
2000WO-US25678.
2000WO-US35678.
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  97US-069694P.
97US-06969B7.
97US-069702P.
97US-069870P.
97US-069871P.
97US-069817P.
98US-070440P.
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97US-069278P.
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The invention relates to an isolated human PRO polypeptide and the polymucleotide encoding it. The PRO polypeptides and nucleic acids are cuseful in diagnosing or treating neurodegenerative disorders such as Alzheimer's disease or Parkinson's disease, and neural damage, e.g. due to trauma or after chemotherapy, inflammatory disease, organ failure, captured at the consist the complications and mutations in general. The gaing, AIDS, diabetic complications and mutations in general. The captured aging, AIDS, diabetic complications and mutations in general. The complete same useful for diagnosing tumours, or for inhibiting the growth of tumour cells. The polypeptides are also useful for wound the healing and associated therapies concerned with re-growth of tissue. The polypeptides are also useful in generating antisense RNA and DNA. PRO cutofic sequences may be used as hybridisation probes in concerned concerned acids are also useful in preparing PRO polypeptides, in assays to identify other proteins or molecules involved in binding reactions, and to generate transgenic or knockout animals, which in turn are useful in the development and screening of therapeutically useful reagents for chromosome identification and tissue typing. The PRO sequences are also useful in gene therapy and as molecular weight markers for protein celectrophoresis purposes. Sequences ABU67121-ABU67136 represent human PRO polypeptides of the invention.
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Best Local Similarity
Matches 175; Conserv
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Hillan KJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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22-DEC-1998; 98US-113296P.
28-JUL-1999; 99US-146222P.
25-WAY-2001; 2001US-0866028.
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                                                                                                                                                                                                                                                                                               LTRVPGGLAEHKYIQVVYLHNINISVVGSSDFCPFGHNTKKASYSGVSLFSNPVQYWBIQ
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PATERCYLSRMSVQLGNF 377
                                                                                            LKKI PSGLPELKYLQI I FLHSNSI ARVGVNDFCPTVPKMKKSLYSA I SLFNNPVKYWEMQ
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                                               PSTFRCVYVRSAIQLGNY 328
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A, Godowski PJ, Grimaldi JC, Gurn
Napier MA, Roy MA, Tumas D, Woo
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2000WO-US00219. 2000WO-US00277. 2000WO-US00376.

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ID ABUS991

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AC ABUS991

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XX ID Novel

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28-AUG-1998
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17-SEP-1998
29-OCT-1998
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05-JAN-1999;
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20-NOV-1998
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2001US-0931836.
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Baker KP, Gerritsen Smith V, Stewart Beresini M, ME, Goddard Stewart TA, A, Go Tumas Deforge L, Desnoyers L, Filvaroff E, G A, Godowski PJ, Gurney AL, Sherwood S; Tumas D, Watanabe CK, Wood WI, Zhang Z; Gao

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WPI; 2003-148238/14. N-PSDB; ABX89304.

and Novel isolated el isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346 PRO1375, which stimulate proliferation of stimulated T-lymphocytes therapeutically useful for enhancing immune response and in cancer

Claim 12; Fig 328; 659pp; English.

invention describes an isolated human PRO polypeptide. The PRO

CC useful for treating cardiac insufficiency disorders. PRO1136 and PRO1186 CC stimulate adrenal cortical capillary endothelial growth, and PRO336, CC PRO343, PRO828, PRO826, PRO1068 or PRO355, PRO826, PRO819, PRO8126, PRO819, PRO819, PRO8196, PRO819, PRO8196, PRO polypeptides are useful in detecting PRO polypeptides in a sample, in linking a bloactive molecule to a cell expressing a PRO polypeptide, and in modulating at least one biological activity of a cell expressing a PRO polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186 Sequence proliferation and/or redifferentiation of chondrocytes in culture are thus useful for treating sports injuries, and arthritis. This is the amino acid sequence of a novel human PRO protein. 379 AA;

밁 S 밁 8 밁 á 맑 δ 밁 Ś Matches 175; Query Match Best Local 181 300 251 240 191 131 121 71 61 11 Similarity EITKVRKVTFNGLNOMIVIELGTNPLKSSGIENGAFQGMKKLSYIRIADTNITSIPQGLP FKNLKNLHALILVNNKISKVSPGAFTPLVKLERLYLSKNQLKELPEKMPKTLQELRAHEN 130 LKKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQ LTRVPGGLAEHKYIQVVYLHNNNISVVGSSDFCPPGHNTKKASYSGVSLFSNPVQYWEIQ FKGLTSLYGLILMNNKLTKIHFKAFLTTKKLRRLYLSHNQLSEIPLNLFKSLAELRIHEN PODRDFEPSIGPVCPFRCQCHLRVVQCSDLGLDKVPKDLPPDTTLLDLQNNKITEIKOGD PSTFRCVYVRSAIQLGNY 328 PRSHFFFFDLFFMCFFGCQCYSRVVHCSDLGLTSVFTNI FFDTRMLDLQNNKIKEIKEND Conservative 55.18; 60; Score 943.5; DB 24; Pred. No. 3.2e-76; 50; Mismatches 82; 24; Length 379; Indels ۳. Gaps 120 70 190 180 359 299 250 239

Search completed: February Job time : 81 secs 9 2004, 11:35:56

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PATERCYLSRMSVQLGNF 377

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Title:
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hypothetical prot adenylate cyclase	garp precursor	hypothetical	hypothetical	platelet membrane	osteoglycin precur	tlr protein	hypothetical	gene wheeler	lysine carboxypep	proteoglycan Lb	proteoglycan-Lb	hypothetical	ingulin-like	insulin-like

## ALIGNMENTS

#  #  #  #  #  #  #  #  #  #  #  #  #  #	THEUTIN-TIME STOWC
210/1. 2/0/2.	
A; ross-reterences: GDB:119839; ONIM:125255	neuronal leucine-r
A;Gene: GDB:DCN	G protein-coupled
C;Genetics:	glial cell membran
C; Comment: This protein binds type I collagen.	chondroadherin pre
	orphan G protein-c
A/Molecule type: protein	fibromodulin - chi
A; Accession: S05640	secreted leucine-r
	omodulin p
A:Title: Dermatan sulphate proteoglycans of human articular cartilage. The properties	protein
Biochem J. 262, 823-827, 1989	slit protein 2 pre
	fibromodulin precu
A: Cross-references: CB:M14219: NID:c181169: PIDN:AAB00774.1: PID:c181170	MEGFS protein - ra
A; MOLECULE CYDE: mkwA  A.Posidines: 1.356 / XPI'.	slit-1 protein hom
A/ACCESSION: A26476	lumican precursor
A; Reference number: A26476; MUID:87017013; PMID:3484330	lumican precursor
A; Title: Primary structure of an extracellular matrix proteoglycan core protein deduc	proline- arginine-
Proc. Natl. Acad. Sci. U.S.A. 83, 7683-7687, 1986	biglycan precursor
R;Krusius, T.; Ruoslahti, E.	biqlycan precursor
A: Note: sequence extracted from NCBI backbone (NCBID:125017)	proteoglycan I - m
A: Residues: 296-359 «DAN»	biglycan precursor
A.Molecule type. DNA	decorin precureor
A;Accession: B45015	
A; Note: sequence extracted from NCB1 backbone (NCB1P:125013)	decorin - rabbit
A;Cross-references: GB:M98262	
A;Residues: 28-70 <da2></da2>	
A; Molecule type: DNA	
A;Status: not compared with conceptual translation	Description
A/Accession: A45015	
A; Reference number: A45015; MUID:93162642; PMID:8432526	
A-Mithle. The himman deportin genee intron-exon promatization, discovery of two alternati	
K; danie180n, K.G.; razzio, A.; conen, 1.; camizzaro, u.A.; BichBeletei, 1.; 10220, s	discribution.
A; Note: sequence extracted from NCBI backbone (NCBIP:125061)	e result being printed,
A;Cross-references: GB:L01125; GB:L01126; GB:L01127; GB:L01128; GB:L01129; GB:L01130;	y chance to have a
A; Residues: 1-359 <vet></vet>	
A;ACCESSION: A45U16	
A;Reference number: A45016; MUID:93162643; PMID:8432527	
A; Title: Human decorin gene: intron-exon junctions and chromosomal localization.	
Genomics 15. 161-168. 1993	
C;ACCESSION: A45015; A45015; A46476; SU5540 I W	
C;Date: 30-Jun-1988 #sequence_revision_30-Jun-1988 #text_change 21-Jan-2000	
decorin precursor - numan NJANIternate names: carrilage proteoglycan protein II; DS-PG II; PG40 core protein; pr	
RESULT 1	

Note: the first two Superfamily: decoring

introns occur before the initiator codon

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F;31-359/Product decorin #status predicted <MPTS
F;48-72/Domain: proteoglycan amino-terminal homology <PAH>
F;48-72/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F;06-129/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;106-129/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;106-129/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;107-129/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F;175-200/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F;201-221/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F;246-269/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F;246-269/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F;270-292/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F;293-316/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F;308-359/Domain: leucine-rich alpha-2-glycoprotein repeat homolog
decorin precursor - bovine

N;Alternate names: dermatan sulfate proteoglycan II; proteoglycan core protein II

C;Species: Bos primigenius taurus (cattle)

C;Datte: 31-Mar-1990 #sequence revision 31-Mar-1990 #text_change 20-Aug-1999

C;Datte: 31-Mar-1990 #sequence revision 31-Mar-1990 #text_change 20-Aug-1999

C;Accession: S06280; B31430; A26545; A20935

R;Day, A.A.; McQuillan, C.I.; Termine, J.D.; Young, M.R.

Biochem. J. 248, 801-805, 1987

A;Title: Molecular cloning and sequence analysis of the cDNA for small proteoglycan A;Reference number: S06280; MUID:88133946; PMID:3435485

A;Accession: S06280

A;Accession: S06280; MUID:88133946; PMID:3435485

A;Cross-references: RMBL:Y00712; NID:g618; PIDN:CAA68702.1; PID:g619

A;Cross-references: EMBL:Y00712; NID:g618; PIDN:CAA68702.1; Neame, P.J.

B;Choi, H.U.; Johnson, T.L.; Pal, S.; Tang, L.H.; Rosenberg, L.; Neame, P.J.

B;Choi, H.U.; Johnson, T.L.; Pal, S.; Tang, L.H.; Rosenberg, L.; Neame, P.J.

A;Reference number: A31430; MUID:89123388; PMID:2914936

A;Accession: B31430

A;Molecule type: protein
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F;211,262,303/Bindi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Mai
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Pred. No. 9.5e-118;
0; Mismatches 0;
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RyChopra, R.K.; Pearson, C.H.; Pringle, G.A.; Fackre, D.S.; Scott, P.G.
Blochem, J. 232, 277-279, 1985

A,; Title: Dermatan sulphate is located on serine-4 of bovine skin proteodermatan sulphate is located on serine-4 of bovine skin proteodermatan sulphate is located on serine-4 of bovine skin proteodermatan sulphate: Dermatan sulphate is located on serine-4 of bovine skin proteodermatan sulphate is proteoglycans.

A; Contents: annotation; glycosylation

C; Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglyc; Keywords: chondroith sulfate proteoglycan; collagen binding; dermatan sulfate; ext F;1-15/Domain: propeptide #status predicted <BRO>
F;16-30/Domain: propeptide #status predicted <BRO>
F;11-36/Product decorin #status predicted <ANT>
F;49-73/Domain: proteoglycan amino-terminal homology <LRR2>
F;107-130/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;107-130/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F;176-199/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F;202-222/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F;203-246/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F;204-108/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F;204-108/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F;204-108/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F;204-1
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A;Title: The dermatan sulfate proteoglycans of bovine sclera A;Reference number: A26545; MUID:87137687; PMID:3818667 A;Accession: A26545
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A; Residues: 31-50 < COS>
A; Residues: 31-50 < COS>
A; Experimental source: sclera
R; Pearson, C.H.; Winterbottom, N.; Fackre, D.S.; Scott,
G. Biol. Chem. 258, 15:101-15:104, 1983
J. Biol. Chem. 258, 15:101-15:104, 1983
A; Reference number: A20935; MUID:84087911; PMID:6654908
A; Accession: A20935
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A;Experimental source: cartilage:
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A; Residues: 31-54 < PEA>
A; Experimental source: skin
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A;Cross-references: GB:S76584; NID:g913374; PIDN:AAB33083.1; PID:g913375
C;Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology;
F;49-73/Domain: proteoglycan amino-terminal homology <PAH>
F;33-106/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F;107-130/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;131-151/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;152-175/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;152-175/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;16-199/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F;202-222/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F;23-246/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F;247-270/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F;271-293/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F;271-293/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F;294-308/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F;309-360/Domain: proteoglycan carboxyl-terminal homology <PCH>
                                                                            N;Alternate names: corneal chondroitin/dermatan sulfate proteoglycan C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 20-Aug-1999
C;Accession: S24317; S58474; S22197
R;Li, W.; Vergnes, J.P.; Cornuet, P.K.; Hassell, J.R.
Arch. Biochem. Biophys. 296, 190-197, 1992
A;Title: cDNA clone to chick corneal chondroitin/dermatan sulfate proteoglycan reveals A;Reference number: S24317; MUID:92296755; PMID:1605630
A;Accession: S24317
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Invest. Ophthalmol. Vis. Sci. 36, 206-215,
A;Title: Cloning and in situ hybridization
A;Reference number: I47020; MUID:95122319;
A;Accession: I47020
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A; Residues: 1-357 <LIW>
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Cross-references: EMBL:X63797; NID:g62887; PIDN:CAA45318.1; PID:g62888
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; PMID:7822148
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A;Molecule type: protein
A;Rolecule type: protein
A;Residues: 31-33,'X',35-39,'X',41-48,'X',50-51 <LIA>
A;Residues: 31-33,'X',35-39,'X',41-48,'X',50-51 <LIA>
C;Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglyca
C;Keywords: collagen binding; extracellular matrix; glycoprotein
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F;288-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
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F;281-305/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
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F;291-305/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F;306-357/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
                                                         A;Cross-references: GB:X53929; NID:g53668; PIDN:CAA37876.1; PID:g53669 R;Naitch, Y.; Suzuki, S. submitted to the EMBL Data Library, July 1990 A;Description: Nucleotide sequences of cDNAs encoding mouse PGI and PG:
                                                                                                                                                                                                                                                                    N;Alternate names: proteoglycan II
C;Species: Mus musculus (house mouse)
C;Date: 24-Feb-1995 #sequence_revision 24-Feb-1995 #text_chan
C;Accession: A55454; S20812
R;Scholzen, T.; Solursh, M.; Suzuki, S.; Reiter, R.; Morgan,
J. Biol. Chem. 269, 28270-28281, 1994
A;Title: The murine decorin. Complete cDNA cloning, genomic cA;Reference number: A55454; MUID:95050610; PMID:7961765
A;Accession: A55454
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A;Molecule type: mRNA
A;Residues: 1-354 <SCH>
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A; Reference number: $20811
A; Accession: $20812
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Pred. No. 3.3e-96;
8; Mismatches 37
                                                                                                                                                                                                                                                                                                          cloning, genomic organization,
pMID:7961765
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F;17-100/Domain: proteoglycan amino-terminal homology <PAH>
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F;217-240/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR
F;241-264/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR
F;265-287/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR
F;288-302/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR
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F;303-354/Domain: proteoglycan carboxyl-terminal homology <PCH>
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A;Cross-references: EME:Z12298; NID:g57549; PIDN:CAA78170.1;
R;Asundi, V.K.; Dreher, K.L.
R;Asundi, V.K.; Dreher, K.L.
Eur. J. Cell Biol. 59, 314-321, 1992
Eur. J. Cell Biol. 59, 314-321, 1992
A;Title: Molecular characterization of vascular smooth muscle A;Reference number: 160238; MUID:93154359; PMID:1493796
A;Accession: 160238
                                                                                                                                                                                                                                                                                                                                                                                                         N;Alternate names: dermatan sulfate proteoglycan-II C;Species: Rattus norvegicus (Norway rat) C;Date: 13-Jan-1995 #sequence revision 13-Jan-1995; C;Accession: S29145; I60238; S28517
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A;Residues: 1-354 <NAI>
A;Cross-references: EMBL;X53929; NID:g53668; PIDN:CAA37876.1; PID:g53669
C;Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology
C;Keywords: collagen binding; extracellular matrix; glycoprotein
C;Keywords: collagen binding; extracellular matrix; glycoprotein
C;Ta-16/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                            R;Abramson, S.R.; Woessner Jr., J.F.
Biochim. Biophys. Acta 1132, 225-227, 1992
A;Title: cDNA sequence for rat dermatan sulfate proteoglycan-II
A;Reference number: S29145; MUID:93003331; PMID:1390895
A;Accession: S29145
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  A; Molecule type: mRNA
A; Residues: 11-354 < RES>
A; Cross-references: EMBL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RELHLDNNKLTRVPGGLAEHKYIQVVYLHNNNISVVGSSDFCPPGHNTKKASYSGVSLFS 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ITSIPQGLPPSLTELHLDGNKISRVDAASLKGLNNLAKLGLSFNSISAVDNGSLANTPHL
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  NID:g56056; PIDN:CAA42519.1;
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Pred. No. 1.4e-92;
B; Mismatches 33;
                                                                       GB/EMBL/DDBJ
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PID:956057
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<LRR4>
<LRR5>
<LRR6>
<LRR7>
<LRR8>
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C;Genetics:
A;Gene: DCN
C;Superfamily: decorin; leucine-rich alpha-2-glycoprotein repea
C;Keywords: collagen binding; extracellular matrix; glycoprotei
C;Keywords: collagen binding; extracellular matrix; glycoprotei
F;1-30/Domain: signal sequence (fragment) #status predicted <SI
A;Cross-references: GB:U17834; NID:g600497; PIDN:AAA58797.1; PID:g600498
C;Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglyc C;Keywords: chondroith sulfate proteoglycan; dermatan sulfate; extracellular matrix; F:1-16/Domain: signal sequence #status predicted <SIG>F:1-37/Domain: propeptide #status predicted <PRO>F;17-37/Domain: propeptide #status predicted <PRO>F;38-369/Product: biglycan #status predicted <PRO>F;38-369/Product: biglycan #status predicted <PRO>F:58-82/Domain: proteoglycan amino-terminal homology <PAH>F:58-82/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>F:116-139/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>F:140-160/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
                                                                                                                                                                                                                                                                                                                                                  R;Dreher, K.L.; Asundi, V.; Matzura, D.; Cowan, K.
Eur. J. Cell Biol. 53, 296-304, 1990
A;Title: Vascular smooth muscle biglycan represents a hi
A;Reference number: S32793; MUID:91184222; PMID:2081545
A;Accession: S32793
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-369 <DRE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 7
$32793
biglycan precursor - rat
N;Alternate names: dermatan sulfate proteoglycan I (DS-PGI); proteoglycan I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;105-14/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;125-145/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;146-169/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;170-193/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;170-193/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;196-216/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F;217-240/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F;241-264/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F;265-287/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F;265-287/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F;268-302/Domain: leucine-rich alpha-2-glycoprotein repeat homology <HR89>
F;265-287/Domain: leucine-rich alpha-2-glycoprotein repeat homology <HR89>
F;268-302/Domain: proteoglycan carboxyl-terminal homology <PCH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Accession: S32793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Species: Rattus norvegicus (Norway rat);Date: 02-Dec-1993 #sequence_revision 01
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Pred. No. 4.3e-90;
3; Mismatches 37;
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A;Cross-references: EMBL:X53928; NID:g53666; PIDN:CAA37875.1; PID:g53667 R;Wegrowski, Y.; Pillarisetti, J.; Danielson, K.G.; Suzuki, S.; Iozzo, R. Genomics 30, 8-17, 1995 A;Title: The murine biglycan: complete cDNA cloning, genomic organization A;Reference number: A57645; MUID:96129295; PMID:8595907 A;Accession: A57645
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A;Title: A dinucleotide repeat in the mouse biglycan gene A;Reference number: I49534; MUID:94319093; PMID:8043960 A;Accession: I49534 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA
                                                                                                           A;Cross-references: GB:L20276; NID:g348961; PIDN:AAA64360.1; PID:g348962
A;Note: authors translated the codom TGG for residue 58 as Cys
R;Rau, W.; Just, W.; Vetter, U.; Vogel, W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Naitoh, Y.; Suzuki, S. submitted to the EMBL Data Library, A;Description: Nucleotide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Aug-1999
C;Catesion: Scall; A57645; T49534
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A;Residues: 1-369 <NAI>
A;Cross-references: EMB
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A; Accession: $20811
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A; Residues: 1-67, 'W',
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/ #status
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A;Cross-references: EMBL:LO7953; NID:g162746
A;Experimental source: aortic smooth muscle
R;Marcum, J.A.; Torok, M.; Evans, S.
submitted to the EMBL Data Library, December 19
A;Reference number: S34229
A;Accession: S34229
A;Molecule type: mRNA
A;Residues: 1-250,'V', 252-369 <MAR>
A;Readeus: 1-250,'V', 252-369 <MAR>
A;Reame, P.J.; Choi, H.U.; Rosenberg, L.C.
J. Biol. Chem. 264, 8653-8661, 1989
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F;140-140/Domain: leucine-rich alpha-2-glycoprotein repeat homology
F;161-184/Domain: leucine-rich alpha-2-glycoprotein repeat homology
F;185-208/Domain: leucine-rich alpha-2-glycoprotein repeat homology
F;210-230/Domain: leucine-rich alpha-2-glycoprotein repeat homology
F;211-254/Domain: leucine-rich alpha-2-glycoprotein repeat homology
F;231-254/Domain: leucine-rich alpha-2-glycoprotein repeat homology
F;279-301/Domain: leucine-rich alpha-2-glycoprotein repeat homology
F;302-316/Domain: leucine-rich alpha-2-glycoprotein repeat homology
F;317-369/Domain: leucine-rich alpha-2-glycoprotein repeat homology
F;317-369/Domain: leucine-rich alpha-2-glycoprotein repeat homology
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S32559
biglycan
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C; Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology;
C; Superfamily: decorin; leucine-rich alpha-2-glycoprotein sulfate; extracellul
C; Keywords: chondroitin sulfate proteoglycan; dermatan sulfate; extracellul
F; 58-82 (Domain: proteoglycan amino-terminal homology <PAH>
F; 58-82 (Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F; 92-115 (Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
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A;Cross-references: GB:L20276; NID:g348961; PIDN:AAA64360.1; PID:g348962
C;Genetics:
                                                                                                                                                                                                                                                                                                                                            biglycan precursor - bovine
N;Alternate names: dermatan sulfate proteoglycan I (DS-PGI); proteochondroitin
C;Species: Bos primidgenius taurus (cattle)
C;Date: 03-May-1994 #Bequence_revision 20-Feb-1995 #text_change 07-May-1999
C;Accession: S32559; S34229: A33701; A31430; PT0078; S55673; A33137
R;Torok, M.A.; Evans, S.A.S.; Marcum, J.A.
Biochim. Biophys. Acta 1173; 81-84, 1993
A;Title: CDNA sequence for bovine biglycan (PGI) protein core.
A;Reference number: S32559; MUID:93250052; PMID:8485158
A;Accession: S32559
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C; Superfamily: decorin;
C; Keywords: chondroitin
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A; Residues: 1-369 < TOR >
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Pred. No. 1.2e-64;
1; Mismatches 86
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dermatan sulfate; extracellular matrix;
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F;58-82/Domain: proteoglycan amino-ferminal homology <PAHS
F;92-115/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F;116-139/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;140-160/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;141-184/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;161-184/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;210-230/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;210-230/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F;231-254/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F;255-278/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F;279-301/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F;302-316/Domain: leucine-rich alpha-2-glycoprotein repeat homology *LRR9>
F;307-369/Domain: leucine-rich alpha-2-glycoprotein repeat homology *LRR9>
F;307-369/Domain: leucine-rich alpha-2-glycoprotein repeat homology *LRR9>
F;317-369/Domain: leucine-rich alpha-2
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A;Residues: 38-187, E',189-367,'Y' <NEA>
A;Residues: 38-187, E',189-367,'Y' <NEA>
A;Residues: 38-187, E',189-367,'Y' <NEA>
A;Residues: 38-187, E',189-367, E',189
Biol. Chem. 264, 2876-2884, 1989
A;Title: Characterization of the dermatan sulfate proteoglycans, A;Reference number: A31430; MUID:89123388; PMID:2914936
A;Accession: A31430
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R;Scott, P.G;; Nakano, T.; Dodd, C.M.
Biochim. Biophys. Acta 1244, 121-128, 1995
A;Title: Small proteoglycans from different regions of
A;Title: Small proteoglycans from different regions of
A;Reference number: S55673; MUID:95284073; PMID:7766647
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A; Residues: 38-41,'X', 43-47,'X', 49-63 <CHO>
A; Note: sequences from skin and cartilage w
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F;210-230/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Molecule type: protein
Residues: 38-41/X',43-47,'X',49-53 <SCO>
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Best Local :
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HLRELHLDNNKLTRVPGGLAEHKYIQVVYLHNNNISVVGSSDFCPPGHNTKKASYSGVSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                     NNKITEIKDGDFKNLKNLHALILVNNKISKVSPGAFTPLVKLERLYLSKNQLKELPEKMP 119
                                                                                                          AKLTGT PKDLPETLNELHLDHNKTQATELEDLLRYSKLYRLGLGHNQTRMIENGSLSFLP
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57.3%; Pred. No. 1.7e-64;
tive 51; Mismatches 87
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A; Map position: Xq28-Xq28
A; Map position: Xq28-Xq28
A; Introns: 80/1; 117/3; 189/1; 226/1; 257/2; 303/3
A; Introns: 80/1; 117/3; 189/1; 226/1; 257/2; 303/3
C; Superfamily: decorin; leucine-rich alpha-2-glycoprotein
C; Keywords: chondroitin sulfate proteoglycan; dermatan sul
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A;Title: Dinucleotide repeat polymorphism at the human biglycan (BGN) locus.
A;Reference number: 138706; MUID:95187185; PMID:7881444
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BGHUN
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A;Residues: 38-41,'X',43-62,'X',64-66
A;Experimental source: bone
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A;Residues: 38-41,'X',43-46,'X',48-57 <ROU>
R;Fisher, L.W.; Hawkins, G.R.; Tuross, N.; Termine, J.D.
J. Biol. Chem. 262, 9702-9708, 1987
A;Title: Purification and partial characterization of small proteoglycans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Roughley, P.J.; White, R.J.
Biochem. J. 262, 823-827, 1989
A;Title: Dermatan sulphate proteoglycans of human articular
A;Reference number: S05639; MUID:90073579; PMID:2590169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-138,'NV',141-162,'DV',165-368 <FIS2>
A;Cross-references: GB:J04599; NID:g184339
A;Note: parts of this sequence, including the amino end of A;Note: the translated sequence in GenBank entry HUMHPGI, r
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A;Title: Deduced protein sequence of bone small proteoglycan I A;Reference number: A32458; MUID:89174714; PMID:2647739
A;Accession: A32458
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C;Date: 21-Apr-1992 #sequence_revision 26-May-1995 #text_change 28-Jan-2000
C;Date: 21-Apr-1992 #sequence_revision 26-May-1995 #text_change 28-Jan-2000
C;Accession: A40757; 138706; A32458; $14349; $05639; A28457
R;Fisher, L.W.; Heegaard, A.M.; Vetter, U.; Vogel, W.; Just, W.; Termine, J. Biol. Chem. 266, 14371-14377, 1991
A;Title: Human biglycan gene. Putative promoter, intron-exon junctions, and A;Reference number: A40757; MUID:91317791; PMID:1860845
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A;Residues: 38-57 <STO>
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A; Residues: 1-368 < FIS1>
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                                                                                                                                        GDB:119727; OMIM:301870
                                                                                                                                                                                                                                                                                                                                                                     MUID:87250639;
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in repeat sulfate; of

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proteoglycan; extracell

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F;1-16/Domain: sign
F;17-37/Domain: pro
F;38-368/Product: b
F;57-81/Domain: pro
F;91-114/Domain: le
F;115-138/Domain: l
                                                                                                                                                                                                                                                                                                                                                                                 proline- arginine-rich end leucine-rich repeat protein PRELP C;Species: Homo sapiens (man) C;Date: 01-Mar-1996 #sequence_revision 01-Mar-1996 "C;Accession: I39068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;115-138/Domain: leucine-rich alpha-2-glycoprotein repeat homology F;160-183/Domain: leucine-rich alpha-2-glycoprotein repeat homology F;160-183/Domain: leucine-rich alpha-2-glycoprotein repeat homology F;160-183/Domain: leucine-rich alpha-2-glycoprotein repeat homology F;184-207/Domain: leucine-rich alpha-2-glycoprotein repeat homology F;209-229/Domain: leucine-rich alpha-2-glycoprotein repeat homology F;230-253/Domain: leucine-rich alpha-2-glycoprotein repeat homology F;278-300/Domain: leucine-rich alpha-2-glycoprotein repeat homology F;278-300/Domain: leucine-rich alpha-2-glycoprotein repeat homology F;316-368/Domain: leucine-rich alpha-2-glycoprotein repeat homology F;316-368/Domain: proteoglycan carboxyl-terminal homology cPCH; F;310,198/Binding site: dermatan sulfate (Ser) (covalent) #status experience f;270,311/Binding site: carbohydrate (Asn) (covalent) #status predic
                                                                               A;Cross-references: GDB:696218
A;Map position: 1q32.1-1q32.1
C;Superfamily: fibromodulin; leucine-rich
C;Keywords: tandem repeat
                                                                                                                                                                                   A;Cross-references: EMBL:U29089; NID:g886135; C;Genetics:
                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-382 <RES>
                                                                                                                                                                                                                                                                                           J. Biol. Chem. 270, 25639-25644, 1995
A;Title: The primary structure of a basic leucine-rich repeat
A;Reference number: 139068; MUID:96029653; PMID:7592739
                                                                                                                                                                                                                                                                                                                                           C;Accession: I39068
R;Bengtsson, E.; Neame, P.J.; Heinegard, D.; Sommarin, J. Biol. Chem. 270, 25639-25644, 1995
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Best Local S
Matches 189
  Query Match
Best Local S
Matches 91
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;38-368/Product: biglycan #status predicted <MAT>
;57-81/Domain: proteoglycan amino-terminal homology <PAH>
;11-11/Domain: leucine-rich alpha-2-glycoprotein repeat
                                                                                                                                                                                                                                                                                                                                                                                                  Species: Homo sapiens (man)
;Species: Homo sapiens (man)
;Date: 01-Mar-1996 #sequence_revision 01-Mar-1996 #text_change
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                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 NITSIPQGLPPSLTELHLDGNKISRVDAASLKGLNNLAKLGLSFNSISAVDNGSLANTPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 TLQELRAHENEITKVRKVTFNGLNOMIVIELGTNPLKSSGIENGAFQGMKKLSYIRIADT
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    91;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NNPVPYWEVQPATFRCVTDRLAIQFGNYK 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LRELHLDNNKLTRVPGGLAEHKYIQVVYLHNNNISVVGSSDFCPPGHVTKKASYSGVSLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNPVQYWEIQPSTFRCVYVRSAIQLGNYK 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KLTGIPKDLPETLNELHLDHNKIQAIELEDLLRYSKLYRLGLGHNQIRMIENGSLSFLPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLVELRIHDNRIRKVPKGVFSGLRNMNCIEMGGNPLENSGFEPGAFDGL-KLNYLRISEA
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  22.5%; ilarity 31.5%; Conservative
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Pred. No. 3.1e-64;
0; Mismatches 88;
  Score 385.5; DB 2;
Pred. No. 1e-20;
9; Mismatches 124;
                                                                                                  alpha-2-glycoprotein
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Ser) (covalent) #status predicted
  (covalent) #status predicted
                                                                                                                                                                                                    PIDN: AAC50230.1;
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y <LRR2>
y <LRR3>
y <LRR4>
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y <LRR6>
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  Gaps
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                                                          HNTKKASYSGVSLFSNPVQYWEIQPSTFRCVYVRSAIQL 325
                                                                                                                                                                                                                       KKLSYIRIADTNITSIPQGLPPSLTELHLDGNKISRVDAASLKGLNNLAKLGLSFNSISA
                                                                                                                                                                                                                                                      NLTEAVGPLPKTLDDLQLSHNKITKVNPGALEGLVNLTVIHLQNNQLKTDSI-SGAFKGL
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                                                                                                                                                                                                                                                                                                                                           GIKYLYLRNNMIBAIEENTFONVTDLQWLILDHNHLENSKIKGRVFSKLKNLKKLHINYN
                                                                                                                                                                                                                                                                                                                                                                     DTTLLDLQNNKITEIKDGDFKNLKNLHALILVNNKI--SKVSPGAFTPLVKLERLYLSKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGI-----GPEVPDDRDFEPSLGP---VCPFRCQCHL---RVVQCSDLGLDKVPKDLPP
                    GPLTYSKITHLRLDGNNLTRADLPQEMYNCLRVAADISL
                                                                                                                                       VDN---GSLANTPHLRELHLDNNKLTRVPGGLAEHKYIQVVYLHNNNISVVGSSDFCPPG
                                                                                                                                                                                 NSLLYLDLSFNQLTKLPTGLPHSLLMLYFDNNQISNIPDEYFQGFKTLQYLRLSHNKLT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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58;

Indels

27;

11

69 51

342

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A;Molecule type: protein
A;Molecule type: protein
A;Residues: 55-76 <BL2>
C;Superfamily: fibromodulin; leucine-rich alpha-2-glycoprotein repeat homology
C;Keywords: glycoprotein; tandem repeat
F;1-18/Domain: signal sequence #status predicted <SIG>
F;1-18/Domain: bignal sequence #status predicted <MAT>
                                                                                                                                                                                                                                                                                                    288 FNISHLIVLHLSHWRISSVP---AINWRLEHLYLWNMSIEKINGTQICP 333
                                                                                                                                                                                                                                                1-343 <BL1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTPHLRELHLDNNKLTRVPGGLAEHKYIQVVYLHNNNISVVGSSDFCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRNIEQIRLSONHISRIPPGVFSKLENLLLLDLOHNRLSDGVFKPDTFHGLKNLMQLNLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chicken
                                                                                                                                                                                                                           GB:M80584
                  21.3%;
Score 365.5; DB 2;
Pred. No. 2.5e-19;
8; Mismatches 146;
                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                284
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                                                                                                                                                                                                                                                                                                                             homolog
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A;Experimental source: cornea (Superiamily: fibromodulin; leucine-rich alpha-2-glycoprotein (Superiamily: fibromodulin; leucine-rich alpha-2-glycoprotein (C;Keywords: glycoprotein; tandem repeat F;1-18/Domain: signal sequence #status predicted <SIG>F;1-9342/Product: lumican #status predicted <MAT>F;92,131,164,256/Binding site: carbohydrate (Asn) (covalent) #s
                                                                                                         RESULT 14
S52284
Lumicon, secretory intersticial proteoglycan precursor -
C;Species: Rattus norvegicus (Norway rat)
C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_
C;Accession: S52284
R;Krull, N.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
A46743
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-338 <KR
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J. Biol. Chem. 265, 8297-8303, 1990
A;Title: Isoforms of corneal keratan sulfate proteoglycan A;Reference number: A35379; MUID:90243714; PMID:2139877
A;Accession: A35379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Sequence and structural implications of a bovine corneal keratan sulfate A;Reference number: A46743; MUID:93280153; PMID:8099356 A;Accession: A46743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N;Alternate names: 37K keratan sulfate-linked protein; corneal keratan sulfate C;Species: Bos primigenius taurus (cattle) C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 24-Sep-1999 C;Accession: A46743; A35379 R;Funderburgh, J.L.; Funderburgh, M.L.; Brown, S.J.; Vergnes, J.P.; Hassell, J.J. Biol. Chem. 268, 11874-11880, 1993
                                                       A; Reference number: A; Accession: S52284
                                                                      A; Reference number: S52284
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                                                                                       Library,
                                                                                       January
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RESULT 15
T42218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 slit-1 protein homolog - rat
N;Alternate names: MEGF4 protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Dec-1999 #sequence_revision 03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomics 51, 27-34, 1998
A; Title: Identification of high-molecular-weight proteins
A; Reference number: Z14126; MUID:98360089; PMID:9693030
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                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Experimental
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FNCNCQLAWLGDWLRKRKIVTGNPRCQNPDFLRQIPLQDVAFPDFRCEEGQEEVGCLPRP
                                                                                                                   LRA---HENEITKVRKVTFNGLNQMIVIELGTNPLKSSGIENGAFQGMKKLS-----
                                                                                                                                                                                                     IK-DGDFKNLKNIHALIIVNNKISKVSPGAFTPLVKLERIYISKNQIKEIPEKMPKTIQE 124
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                                                                                 LRTLMLRNNRISCIHNDSFTGLRNVRLLSLYDNHITT--ISPGAFDTLQALSTLNLLANP 672
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                                                                                                                                                                                                                                                                                                                                                  Score 327.5; DB 2; Pred. No. 1.2e-15;
                                                                                                                                                                                                                                                                                                                               Mismatches
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A;Cross-references: I
C;Genetics:
A;Gene: MEGF5
C;Superfamily: fruit
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A;Accession: T13953
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1523 <NAK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N;Alternate names: slit protein homolog
C;Speciles: Rattus norvegicus (Norway rat)
C;Speciles: Rattus norvegicus (Norway rat)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 16-Aug-2
C;Accession: T1395
C;Accession: T1395
C;Accession: T1395
C;Accession: T1395
C;Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, Ogenomics 51, 27-34, 1998
Genomics 51, 27-34, 1998
A;Title: Identification of high-molecular-weight proteins with multiple
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RESULT 17
S55275
fibromodulin precursor - human
N;Alternate names: 59K collagen-binding matrix protein
C;Species: Homo sapiens (man)
C;Date: 23-Aug-195 #sequence revision 03-Oct-1995 #tea
C;Accession: S55275; S35710; S32752; S41925
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Best Local S
Matches 99
Species: Homo sapiens (man)

Date: 23-Aug-1995 #sequence_revision 03-Oct-1995 #text_change;
Accession: S55275; S35710; S32752; S41925
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSDFCPPGHNTKKASYSGVSLFSNPV 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNNKISSLSNSSFTNMSQLTTLILSYNALQCIPPLAFQGL---RSLRLLSLHGNDVSTLQ 848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SFNSISAVDNGSLANTPHLRELHLDNNKLTRVP----GGLAEHKYIQVVYLHNNNISVVG 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QCPQECACLDTVVRCSNKHLQALPKGIPKNVTELYLDGNQFTLV-PGQLSTFKYLQLVDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GIPRKAFRGVTGVKNLQLDNNHI--SCIEDGAFRALRDLEILTLNNNNISRILVTSFNHM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KVRKVTFNGLNQMIVIELGTNPLKSSGIENGAFQGMXKLSYIRIADTNI-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RVLHLEDNOVSVIERGAFODLKOLERLRLNKNKLOVLPELLFOSTPK-LTRLDLSENQIQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGIF----ADVTSLSHLAIGANPL 868
                                                                                                                                                                                 LLNANKINCLRVNTF-----QDLQNLNLLSLYDNKLQ 416
                                                                                                                                                                                                                         YLHNNNISVVGSSDFCPPGHNTKKASYSGVSLFSNPVQ 305
                                                                                                                                                                                                                                                                                        ASLKGLNNLAKLGLSFNSISAVDNGSLANTPHLRELHLDNNKLTRVPGGLAEHKY-IQVV
                                                                                                                                                                                                                                                                                                                                        GPHSEAPACNANSLSCPSACSCSNNIVDCRGKGLTEIPANLPEGIVEIRLEQNSIKSIPA
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                    24-Sep-1999
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A;Accession: B36665 A;Status: preliminary A;Molecule type: mRNA

A;Reference number: A36665; MUID:91099665; PMID:2176636

J.R.; Goodman, C.S.; Artavanis-Tsakonas,

of midline

glia

and

R;Rothberg, J.M.; Jacobs, J.R.; Goodman, Genes Dev. 4, 2169-2187, 1990 A;Title: slit: an extracellular protein

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A;Gene: GDB:FMOD
A;Gene: GDB:PMOD
A;Gene: GDB:PMOD
A;Gene: GDB:PMOD
A;Gene: GDB:PMOD
A;Gene: GDB:28979; OMIM:600245
A;Map position: 1q32.1-1q32.1
A;Introns: 326/2
C;Superfamily: fibromodulin; leucine-rich alpha-2-glycoprotein repeat homology
C;Evywords: cartilage; chondroitin sulfate proteoglycan; collagen binding; conn
F;1-18/Domain: signal sequence #status predicted <AMIP
F;19-376/Product: fibromodulin #status predicted <MATP
F;38,39,42,45,47,50,53,55,63,65/Binding site: sulfate (Tyr) (covalent) #status
F;317,166,201,291/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Reference number: S55275; MUID:94379985; PMID:8093006
A;Accession: S55275
A:Status.
RESULT 18
B36665
B36665
Ship protein 2 precursor - fruit fly (Drosophila melanogaster)
Shit protein 2 precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:X75546; NID:g453156; PIDN:CAA5323
A;Note: the nucleotide sequence was submitted to the EMBL
R;Antonsson, P.; Heinegard, D.; Oldberg, A.
Biochim. Biophys. Acta 1174, 204-206, 1993
A;Title: Structure and deduced amino acid sequence of the
A;Reference number: S35710; MUID:93363641; PMID:8357838
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-3,'T',5-86,'P',88-209,'N',211-225,'Y',227-343,'Q',345-354,'M',356-362,'E
A;Cross-references: EMBL:X72913; NID:g297090; PIDN:CAAS1418.1; PID:g297091
C;Comment: Keratan sulfate can be covalently attached to N-acetylglucosamine at the as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 236 RKVPDGLPSALEQLYMEHNNVYTVPDSYFRGAPKLLYVRLSHNSLT--NNGLASNTFNSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TSIPQGLPPSLTELHLDGNKISRVDAASLKGLNNLAKLGLSFNSISAVDNGSLANT---P
                                                                                                                                                                                                                               DGNEIKRSAMPADAPLĊLRLASLÍEI
                                                                                                                                                                                                                                                                                                                                          SLLELDLSYNOLOKIP----PVNTNLENLYLOGNRINEFSISSFCTVVDVVNFSKLOVVRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QELRAHENEITKVRKVTFNGLNQMIVIELGTNPLKSSGIENGAFQGMKKLSYIRIADTNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EIKOGDFKNLKNLHALILVNNKIS--KVSPGAFTPLVKLERLYLSKNQLKELPEKMPKTL
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Pred. No. 2.1e-16;
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to the EMBL Data
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Library, No
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F288-313/Domain: proteoglycan amino-terminal homology cPAH2>
F;323-346/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRF
F;347-370/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRF
F;371-394/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRF
F;371-394/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRF
F;371-394/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRF
F;419-442/Domain: proteoglycan carboxyl-terminal homology cRS2>
F;512-537/Domain: proteoglycan amino-terminal homology cRNH3>
F;512-537/Domain: proteoglycan amino-terminal homology cRNH3>
F;547-571/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRF
F;526-619/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRF
F;526-631/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRF
F;620-643/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRF
F;620-643/Domain: proteoglycan carboxyl-terminal homology cRST
F;743-766/Domain: proteoglycan amino-terminal homology cRST
F;743-766/Domain: proteoglycan amino-terminal homology cRRH4>
F;743-766/Domain: proteoglycan carboxyl-terminal homology cRRH4>
F;767-790/Domain: proteoglycan carboxyl-terminal homology cRRH4>
F;768-790/Domain: proteoglycan carboxyl-terminal homology cRRF>
F;1028-1061/Domain: BGF homology cRFP>
F;1028-1061/Domain: BGF homology cRFP>
F;1028-1061/Domain: BGF homology cRFP>
F;1048-109/Domain: BGF homology cRFP>
RESULT 19
A36665.

slit protein 1 precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 30-Apr-1991 #sequence revision 30-Apr-1991 #text_chang
C;Accession: A36665; A31640; S13523
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KNPFICDCNLRWLADYLHKNPIETSGARCESPKRMHRRRIESLREEKFKCSWGELRMKLS
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                                                                                                                                                                                                                                                       QISCV-----MPGSFEHLNSLTSLNLASNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSIRLLLLNANEISCIRKDAFRDLHSLSLLSLYDNNIQS--LANGTFDAMKSMKTVHLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KCSGLTEHAPMECGAENS----CPHPCRCADGIVDCREKSLTSVPVTLPDDTTDVRLEQN
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                       revision 30-Apr-1991 #text_change 02-Aug-2002
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Pred. No. 2.4e-15;
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Best Local s
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                       451
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                KNPFICDCNLRWLADYLHKNPIETSGARCESPKRMHRRRIESLREEKFKCSWGELRMKLS
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F;00-31/Domain: Proteogly Year animor-terminal nombody *Frant*
F;101-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology < LRR
F;125-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology < LRR
F;125-146/Domain: leucine-rich alpha-2-glycoprotein repeat homology < LRR
F;127-196/Domain: leucine-rich alpha-2-glycoprotein repeat homology < LRR
F;127-220/Domain: leucine-rich alpha-2-glycoprotein repeat homology < LRR
F;127-220/Domain: leucine-rich alpha-2-glycoprotein repeat homology < LRR
F;228-272/Domain: leucine-rich alpha-2-glycoprotein repeat homology < LRR
F;371-394/Domain: proteoglycan carboxyl-terminal homology < LRR
F;371-571/Domain: proteoglycan carboxyl-terminal homology < LRR
F;450-649/Domain: leucine-rich alpha-2-glycoprotein repeat homology < LRR
F;572-595/Domain: leucine-rich alpha-2-glycoprotein repeat homology < LRR
F;572-595/Domain: leucine-rich alpha-2-glycoprotein repeat homology < LRR
F;620-643/Domain: leucine-rich alpha-2-glycoprotein repeat homology < LRR
F;673-30/Domain: proteoglycan carboxyl-terminal homology < LRR
F;784-786/Domain: leucine-rich alpha-2-glycoprotein repeat homology < LRR
F;791-884/Domain: leucine-rich alpha-2-glycoprotein repeat homology < LRR
F;108-108/Domain: leucine-rich alpha-2-glycoprotein repeat homology < LRR
F;108-108/Domain
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A;Residues: 1-1480 <ROT>
A;Cross-references: GB:X53959; NID:g8614; PIDN:CAA37910.1; PID:g861
A;Cross-references: GB:X53959; NID:g8614; PIDN:CAA37910.1; PID:g861
A;Cross-references: GB:X53959; NID:g8614; PIDN:CAA37910.1; PID:g861
A;Cross-references: GB:X53959; NID:g8614; PID:GAA37910.1; PID:g861
A;Coll 55; 1047-1059; 1988
A;Title: slit: An EGF-homologous locus of D. melanogaster involved
A;Paference number: A31640; MUID:89077533; PMID:3144436
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A;Introns: 1351/3
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A;Residues: 881-1182,'G',1185-1404,'GT',1463-1464,'YHA'
A;Cross-references: GB:M23543; NID:g340939; PID:g514357
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4, 2169-2187, 1990
                                                                                                                                                                                                                                                                                                                                                                                                          2 EASGIGPEVPDDRDFBPSLGPVCPFRCQCHLRVVQCSDLGLDKVPKDLPPDTTLLDLQNN
                                                                 LQBLR----AHENEITKVRKVTFNGLNQMIVIELGTNPLKSSGIENGAFQGMKKLSYIRIA
                                                                                                                                                                                                          FITELPPKSFSSFRRLRRIDLSNNNISRIAHDALSGLKQLTTLVLYGNKIKDLPSGVFKG
                                                                                                                                                                                                                                                                KITBIKDGDFKNLKNLHALILVNNKISKVSPGAFTPLVKLERLYLSKNQLKELPEKMPKT
                                                                                                                                                                                                                                                                                                                                                KCSGLTEHAPMECGAENS----CPHPCRCADGIVDCREKSLTSVPVTLPDDTTDVRLEQN
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homology <EGF1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 323; DB 2;
Pred. No. 2.4e-15;
1; Mismatches 129
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akonas, S.
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R;Plaas, A.H.K.; Neame, P.J.; Nivens, C.M.; Reiss, L.
J. Biol. Chem. 265, 20634-20640, 1990
A;Title: Identification of the keratan sulfate attachment sites on bovine fibromodulin. A;Reference number: A23663; MUID:91056119; PMID:2243109
A;Contents: annotation; keratan sulfate attachment
C;Comment: Keratan sulfate can be covalently attached to N-acetylglucosamine at the aspa C;Superfamily: fibromodulin; leucine-rich alpha-2-glycoprotein repeat homology
C;Keywords: cartilage; chondroitin sulfate proteoglycan; collagen binding; connective ti F;1-18/Domain: signal sequence #status predicted <SIGS
F;19-375/Product: fibromodulin #status predicted <SIGS
F;19-175/Product: fibromodulin #status predicted (Tyr) (covalent) #status predicted
F;38,42,45,47,50,53,62,64/Binding site: sulfate (Tyr) (covalent) #status experimental
                                                                               RESULT 21
T42626
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C;Date: 22-Jan-1993 #text_change
C;Date: 22-Jan-1993 #text_change
C;Accession: S05390; S26942; S06040
R;Oldberg, A.; Antonsson, P.; Lindblom, K.; Heinegard, D.
EMBO J. 8, 2601-2604, 1989
A;Title: A collagen-binding 59-kd protein (fibromodulin) is stru
A;Reference number: S05390; MUID:90060020; PMID:2531085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fibromodulin precursor - bovine fibromodulin precursor - bovine N;Alternate names: 59K collagen-binding matrix protein N;Alternate names: 59K collagen 
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A; Residues: 90-105;190-199;274-281 <OL2>
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A; Accession: S26942
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A; Residues: 1-375 <OLD>
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secreted leucine-rich repeat-containing protein SLIT2 - mouse N; Alternate names: neurogenic extracellular slit protein
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Pred. No. 1.6e-15;
5; Mismatches 120;
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RESULT 22
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C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 16-Aug-2002
C;Accession: T42626
R;Holmes, G.P.; Negus, K.; Burridge, L.; Raman, S.; Algar, E.; Yamada, T.; Little, Mech. Dev. 79, 57-72, 1998
A;Title: Distinct but overlapping expression patterns of two vertebrate slit homolo A;Reference number: 222177; MUID:99279238; PMID:10349821
                                                                                                                                                           A;Cross-receiver.
C;Superfamily: fibromodulin;
                                                                                                                                                                                                                                                                                                             Biochem. J. 317, 785-789, 1996
A; Title: Differential expression of fibromodulin mRNA associated A; Reference number: S71876; MUID:96332470; PMID:8760363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: Slit2
C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Gallus gallus (chicken)
C;Date: 14-Feb-1997 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-1025 < HOL>
                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-380 < NUR>
                                                                                                                                                                                                                                                                                          A; Accession: S71876
                                                                                                                                                                                                                                                                                                                                                                                 R; Nurminskaya, M.V.; Birk, D.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references:
                                                                                                                                                                                                                                                                   A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: S71876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fibromodulin -
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                                                                                       Query Match
Best Local Similarity
Matches 81; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          242 KYLPKGIPKDYTELYLDGNQFTLV-PKELSNYKHLTLIDLSNNRISTLSNQXFSNMTQLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      299 LFSNPV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 FIGLGSVRLLSLYDNOITTVAPGAFDXLHSLSTLNLLANPFNCNCHLAWLGEWLRRKRIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83 VNNKISKVSPGAFTPLVKLERLYLSKNQLKELPEKMPKTLQELRA-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 CPFRCQCHLRVVQCSDLGLDKVPKDLPPDTTLLDLQNNKITEIK-DGDFKNLKNLHALIL
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CPQECDCPPNFSSAMYCDTRNLRYLP-FVPTRMKYVYFQNNQITAIQEGAFDNATELEWL
                                          CPFRCQC---HLRVVQCSDLGLDKVPKDLPPDTTLLDLQNNKITEIKDGDFKNLKNLHAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELHLDNNKLTRVP----GGLAEHKYIQVVYLHNNNISVVGSSDFCPPGHNTKKASYSGVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IGANPLYCDCNMQWLSDWVKSEYKE--PGIARC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGNPRCQKPYFLKEIPIQDVAIQDFTCDDGNDDNSCSPLSRCPSECTCLDTXVRCSNKGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein
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                                                                                                                                                                           MBL:U34977; NID:g1098905; PIDN:AAC60016.1; PID:g1098906
omodulin; leucine-rich alpha-2-glycoprotein repeat homolo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL: AF074960; NID: g4151258; PID: g4151259;
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                                                                                         50;
                                                                                       Score 298.5; |
Pred. No. 2.4e
50; Mismatches
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Pred. No. 6.7e-15;
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                                                                                                              5; DB 2;
2.4e-14;
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                                                                                         119;
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RESULT 24
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C;Comment: This protein is a receptor for a novel class of glycoprotein ligands.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-907 < MCD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;McDonald, T.; Wang, R.; Bailey, W.; Xie, G.; Chen, F.; Caskey, C.T.; Liu, Biochem. Biophys. Res. Commun. 247, 266-270, 1998
A;Title: Identification and cloning of an orphan G protein-coupled receptor A;Reference number: JE0176; MUID:98308104; PMID:9642114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  orphan G protein-coupled receptor precursor - human C;Species: Homo sapiens (man) C;Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 21-Jul-2000 C;Accession: JE0176
                                                                                                                                                                                                                                                                                                                                                                          S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: HG38
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Best Local S
Matches 82
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                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                            RVP-GGLAEHKYIQVVYLHNNNISVVGSSDF
                                                                                                                                                                      LTELHLDGNKI SRVDAASLKGLNNLAKLGLSFNSI SAVDNGSLANTPHLRELHLDNNKLT
                                                                                                                                                                                                                                     RKVTFNGLNQMIVIELGTNPLKSSGIENGAFQGMKKLSYIRIADTNITSIPQ---
                                                                            SIPEKAFVGNPSLITIHFYDNPIQFVGRSAF
                                                                                                                                                                                                      PPSCFSGLHSLRHLWLDDNALTEIPVQ--AFRSLSALQAMTLALNKIHHIPDYAFGNLSS
                                                                                                                                                                                                                                                                                                                                      CPTHCHCEPDGRMLLRVDCSDLGLSELPSNLSVFTSYLDLSMNNISQLLPNPLPSLRFLE
                                                                                                                                                                                                                                                                                                                                                                     CPFRCQCH-----LRVVQCSDLGLDKVPKDLPPDTTLLDLQNNKITEIKDGDFKNLKNLH 78
                                                                                                                                         LVVLHLHNNRIHSLGKKCFDGLHSLETLDLNYNNLDEFPT-AIRTLSNLKELGFHSNNIR
                                                                                                                                                                                                                                                                       ELRLAGNALTYIPKGAFTGLYSLKVLMLQNNQLRHVPTEALQNLRSLQSLRLDANHISYV
                                                                                                                                                                                                                                                                                                      ALILVNNKISKVSPGAFTPLVKLERLYLSKNOLKELPEKM---PKTLQELRAHENEITKV 135
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precursor
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Pred. No. 1.3e-
50; Mismatches
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d <IM1>
d <IM2>
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A;Molecule type: mrNA
A;Residues: 1-1091 <SUZ>
A;Residues: 1-1091 <SUZ>
A;Cross-references: GB:D78572; NID:g1545806; PIDN:BAA11416.1; PID:g1545807
A;Cross-references: GB:D78572; NID:g1545806; PIDN:BAA11416.1; PID:g1545807
C;Superfamily: leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan
F;36-61/Domain: proteoglycan amino-terminal homology <PAH>
F;36-61/Domain: leucine-rich alpha-2-glycoprotein repeat homology <PAH>
F;11-94/Domain: leucine-rich alpha-2-glycoprotein repeat homology <PAH>
F;18-141/Domain: leucine-rich alpha-2-glycoprotein repeat homology <PAH>
F;166-189/Domain: leucine-rich alpha-2-glycoprotein repeat homology <PAH>
F;166-189/Domain: leucine-rich alpha-2-glycoprotein repeat homology <PAH>
F;214-237/Domain: leucine-rich alpha-2-glycoprotein repeat homology <PAHR>
F;238-261/Domain: leucine-rich alpha-2-glycoprotein repeat homology <PAHRP>
F;238-261/Domain: leucine-rich alpha-2-glycoprotein repeat homology <PAHRP>
F;262-285/Domain: leucine-rich alpha-2-glycoprotein repeat homology <PAHRP>
F;262-285/Domain: leucine-rich alpha-2-glycoprotein repeat homology <PAHRP>
F;263-309/Domain: leucine-rich alpha-2-glycoprotein repeat homology <PAHRP>
F;266-309/Domain: leucine-rich alpha-2-glycoprotein repeat homology <PAHRP>
F;266-285/Domain: leucine-rich alpha-2-glycoprotein repeat homology <PAHRP>
F;266-285/Domain: leucine-rich alpha-2-glycoprotein repeat homology <PAHRP>
F;266-309/Domain: leucine-rich alpha-2-glycoprotein repeat homology <PAHRP>
F;266-285/Domain: leucine-rich
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C;Species: Bos primic
C;Date: 07-Oct-1994 #
C;Accession: A53860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: A58532
R;Suzuki, Y.; Sato, N.; Tohyama, M.; Wanaka, A.; Takagi, T.
Biol. Chem. 271, 22522-22527, 1996
A;Title: cDNA cloning of a novel membrane glycoprotein that A;Reference number: A58532; MUID:96394313; PMID:8798419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       glial cell membrane glycoprotein LIG-1 precursor - mouse C;Species: Mus musculus (house mouse) C;Date: 11-Apr-1997 #sequence_revision 11-Apr-1997 #text_change
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F;300-346/Domain: proteoglycan carboxyl-terminal homology <PCH>
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J. Biol. Chem. 269, 21547-21554, 1994
A;Title: The structure of a 38-kDa leucine-rich protein
A;Reference number: A53860; MUID:94342341; PMID:8063792
A;Accession: A53860
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A; Residues: 1-361 < NEA>
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Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change
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F;310-333/Domain: 1
F;334-357/Domain: 1
F;358-381/Domain: 1
F;385-408/Domain: F;385-408/Domain: P;409-432/Domain: 1
F;440-485/Domain: 1
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A;Residues:
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;Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HLDGNKISRVDAASLKGLNNLAKLGLSFNSISAVDNGSLANTPHLRELHLDNNKLTRV-P 255
                                                                                                                                                                                                                                                                                                       CPFRCQCHL--RV---VQCSDLGLDKVPKDLPPDTTLLDLQNNKITEIKDGDFKNLKNLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNELTAI-PSLGTASIGVVSLFLQHNKILSVDGSQLKSYLSLEVLDLSSNNITEIRSSCF 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NNKISKVSPGAFTPLVKLERLYLSKNOLKELPEKMPK---TLQELRAHENEITKVRKVTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CPFRCQCHLRVVQCSDLGLDKVPKDLPPDTTLLDLQNNKITEIKDGDFKNLKNLHALILV 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGLAEHKYIQVVYLHNNNISVVGSS--DFCPPGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DLNRNR IRL I EGLTFQGLDSLEVLRLQRNN I SRLTDGAFWGLSKMIVLHLEYNSLVEVNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -NGLNOMIVIELGTNPLKSSGIENGAFQGM-KKLSYIRIADTNITSIPQGL--PPSLTEL 196
                                 RVPGGLAEHKYIQ----
                                                                                                                                                                           RKVTFNGLNQMIVIELGTNPLKSSGIENGAFQGMKKLSYIRIADTNITSIPQ---GLPPS
                                                                                                                                                                                                                                               ALILVNNKISKVSPGAFTPLVKLERLYLSKNQLKELPEKM---PKTLQELRAHENEITKV 135
                                                                                                                                                                                                                                                                                     CPSHCHCELDGRMLLRVDCSDLGLSELPSNLSVFTSYLDLSMNNISQLPASILHRLCFLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSLYGLTALHQLHLSNNSISRIQRDGWSFCQKLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PNGLR----IRELNLASNRISILESGAFDGLSRSLLTLRLSKNRITQLPVKAFKLPRLTQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAAACTCAGNSLDCSGRGLATLPRDLPSWTRSLNLSYNRLSEIDSAAFEDLTNLQEVYLN 102
                                                                      LVVLHLHNNRIHSLGKKCFDGLHSLETLDLNYNNLDEFPT-AIKTLSNLKELGFHSNNIR
                                                                                                      LTELHLDGNKISRVDAASLKGLNNLAKLGLSFNSISAVDNGSLANTPHLRELHLDNNKLT 252
                                                                                                                                       PPSCFSGLHSLRHLWLDDNALTDVPVQ--AFRSLSALQAMTLALNKIHHIADYAFGNLSS
                                                                                                                                                                                                              ELRLAGNAL THI PKGAFTGLHSLKVLMLQNNQLRKVPEEALQNLRSLQSLRLDANHI SYV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     leucine-rich alpha-2-glycoprotein repeat homology proteoglycan carboxyl-terminal homology <PCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                  <HER>
ERAFVGNPSLITIHFYDNPIQFVGVSAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Commun. 254, 273-279, 1999
n of a novel seven-transmembrane receptor with homology to 0193; MUID:99121227; PMID:9920770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.0%;
                                                                                                                                                                                                                                                                                                                                                                          16.7%;
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                                   - VVYLHNNNISVVGSSDF
                                                                                                                                                                                                                                                                                                                                                           50;
                                                                                                                                                                                                                                                                                                                                                       Score 285.5; DB 2;
Pred. No. 7e-13;
0; Mismatches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 291; DB 2;
Pred. No. 3.6e-13;
5; Mismatches 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H.C.; Hermans-Borgmeyer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-Jul-1999 #text_change 11-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          287
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301
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RESULT

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27

GAEPGTPGEAE----GPACPATCACSYDDEVNELSVFCSSRNLTRLPDGIPGGTQALWL

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neuronal leucine-rich repeat protein-3 - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002 C;Accession: JCT/63
R;Fukamachi, K.; Matsuoka, Y.; Kitanaka, C.; Kuchino, Y.; Tsuda, H. Biochem. Biophys. Res. Commun. 287, 257-263, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-707 < FUK>
A; Cross-references: GB: AF291437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochem. Biophys. Res. Commun. 287, 257-263, 2001
A,Title: Rat neuronal leucine-rich repeat protein-3: Cloning and regulation
A;Reference number: JC7763; PMID:11549284
A;Contents: Fibrosarcoma cells
                                                                                                                                                                                                                                                                                                                                                                                   RESULT 28
JC5239
S
                                                                                                                                                                                                                                                                                                    insulin-like growth factor acid-labile chain - baboon
c;Species: Papio sp. (baboon)
C;Date: 17-Apr-1997 #sequence_revision 09-May-1997 #text_change
C;Accession: JC5239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: nlrr-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Comment: This protein, a new in protein-protein interaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: JC7763
                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-605 < DEL>
                                                                                                                                                                                                  A;Reference number: JC5239; MUID:97040714; PMID:8886027 A;Contents: liver
                                                                                                                                                                                                                                          Biochem. Biophys. Res. Commun. 227, 897-902, 1996 A; Title: The cloning and expression of the baboon acid-labile
                                                                                                                                                                                                                                                                               R;Delhanty, P.; Baxter, R.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local :
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                                                                                                                        Comment: This factor
                                             Matches
                                                            Query Match
Best Local (
                                                                                                                                                                                  Accession: JC5239
                                                       Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 CPFRCQCHLR-------VVQCSDLGLDKVPKDLPPDTTLLDLQNNKITEIKDG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell adhesion
      ຫ
                                           87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      h 16.5%;
Similarity 28.4%;
                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NGAFQGMKKLSYIRIADTNITSIPQ----GLPPSLTELHLDGNKISRVDAASLKGLNNLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VNHNLLSAISPGAFVGLHNLLRLHLNSNRLQMINSKWFEALPNLEILMLGDNPILR--IK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DPP--VNLTGLDLSQNNLSSVTNINVQKMSQLLSVYLEENKLTELPEKCLYGLSNLQELY
      GIGPEVPDDRDFEPSLGPVCPFRCQC------HLRVVQCSDLGLDKVPKDLPPDTTLLDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FLDLNKNPINRIRRGDFSNMLHLKELGINNMPELVSIDSLAVDNLPDLRKIEATNNPRLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DMNFQPLLKLRSLVIAGINLTEVPDDALVGL-ENLESISFYDNRLNKVPQVALQKAVNLK 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AHENEITKVRKVTFNGLN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEKNIKNIHALIIVNNKISKVSPGAFTPIVKLERIYISKNQIKEIPEKM---PKTIQEIR 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CPQLCTCEIRPWFTPRSIYMEASTVDCNDLGLLNFPARLPADTQILLLQTNNIARIEHST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YLHNNNISVVGSSDFCPPGHNTKKASYSG------VSLFSNPVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KLGLSFNSISAVDNGSLANTPHLRELHLDN-NKLTRVPG----GLAEHKYIQVV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YIHPNAFFRLPKLESLMLNSNALSALYHGTIBSLPNLKEISIHSNPIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                        is structurally related to proinsulin
                                                            15.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            member of the neuronal leucine-rich repeat protein fam and functions as a cell adhesion molecule or soluble l
                                           58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52;
                                                            Score 273;
Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 283.5; DB 2
Pred. No. 6.9e-13;
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                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QMI-----VIELGTNPLKSSGIE
                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126;
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                                                                                Length 605;
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                                           Indels
                                                                                                                      and have insuline-like
                                                                                                                                                                                                                                              subunit of
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                                         52;
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                                         Gaps
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                                                                                                                                                                                                                                              insulin-
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F;123-146/Domain: leucine-rich alpha-2-glycoprotein repeat home F;147-170/Domain: leucine-rich alpha-2-glycoprotein repeat home F;171-194/Domain: leucine-rich alpha-2-glycoprotein repeat home F;171-194/Domain: leucine-rich alpha-2-glycoprotein repeat home F;195-218/Domain: leucine-rich alpha-2-glycoprotein repeat home F;243-266/Domain: leucine-rich alpha-2-glycoprotein repeat home F;267-290/Domain: leucine-rich alpha-2-glycoprotein repeat home F;267-390/Domain: leucine-rich alpha-2-glycoprotein repeat home F;315-338/Domain: leucine-rich alpha-2-glycoprotein repeat home F;315-338/Domain: leucine-rich alpha-2-glycoprotein repeat home F;339-362/Domain: leucine-rich alpha-2-glycoprotein repeat home F;339-366/Domain: leucine-rich alpha-2-glycoprotein repeat home F;387-410/Domain: leucine-rich alpha-2-glycoprotein repeat home F;411-434/Domain: leucine-rich alpha-2-glycoprotein repeat home F;459-482/Domain: leucine-rich alpha-2-glycoprotein repeat home F;459-459/Domain: leucine-rich alpha-2-glycoprotein repeat hom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Structure and functional expression of the acid-labile A;Reference number: A41915; MUID:92357025; PMID:1379671 A;Accession: A41915
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A41915
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C; Superfamily: leucine-rich alpha-2-glycoprotein repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:M86826; NID:g184807; PIDN:AAA36047.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA; I
A; Residues: 1-605 < LEO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;75-98/Domain: leucine-rich alpha-2-glycoprotein repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   insulin-like growth factor-binding complex acid-labile chain N,Alternate names: Acid-Labile Subunit (ALS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Species: Homo sapiens (man);Date: 31-Dec-1993 #sequence
                                                                                                                                                                                                                                                                                                Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Accession: A41915
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                                                                                            QNNKITEIKDGDFKNLKNLHALILVNNKISKVSPGAFTPLVKLERLYLSKNQLKELP---
                                                                                                                                                          GADPGTPGEAE-----GPACPAACVCSYDDDADELSVFCSSRNLTRLPDGVPGGTQALWL
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                                                                                                                                                                                                            GIGPEVPDDRDFEPSLGPVCPFRCQCHL----RVVQCSDLGLDKVPKDLPPDTTLLDL
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-EKMPKTLQELRAHENEITKVRKVTFNGLNQMIVIELGTNPLKSSGIENGAPQGMKKLSY
                                                  DGNNLSSVPPAAFQNLSSLGFLNLQGGQLGSLEPQALLGLENLCHLHLERNQLRSLALGT
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                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                             15.9%; Score 273; 25.8%; Pred. No. 3.
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alpha-2-glycoprotein repeat homology <LRR2>
                                                                                                                                                                                                                                                                       58;
                                                                                                                                                                                                                                                         Pred. No. 3.se
8; Mismatches
                                                                                                                                                                                                                                                                                             .3e-12;
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R;Dai, J.; Baxter, R.C. R;Dai, J.; Baxter, R.C. Biochem. Biophys. Res. Commun. 188, 304-309, 1992
A;Title: Molecular cloning of the acid-labile subunit of a:Reference number: JC1282, MUID:93038676; PMID:1384485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Note: the authors translated the codon AAG for residue 63 as Arg, C;Superfamily: leucine-rich alpha-2-glycoprotein repeat homology F;1-27/Domain: signal sequence #status predicted <SIG>F;28-603/Product: insulin-like growth factor binding protein, acid 1F;267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology
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A;Residues: 1-603 <DAI>
A;Cross-references: GB:S46785; NID:g258002; PIDN:AAB23770.2;
A;Experimental source: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               insulin-like growth factor-binding protein acid labile chain precursor - C;Species: Rattus norvegicus (Norway rat) C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jul-20 C;Accession: JC1282
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 RLAHNAIASL
                                  KKASYSGVSLFSNPVQYWEIQPSTFRCVYVRSAIQLGN
                                                                      FVHLPRLQKLYLDRNLITAVAPGAFLGMKALRWLDLSHNRVAGLMEDTF--PGLLGLHVL
                                                                                                           LANTPHLRELHLDNNKLTRV-PGGLAEHKYIQVVYLHNNNISVVGSSDFCPPG----HNT
                                                                                                                                             VVLPDT----VFQGL-GNLHELVLAGNKLTYLQPALFCGLGELRELDLSRNALRSVKANV
                                                                                                                                                                              IRIADTNITSIPQGLPPSLTELHLDGNKISRVDAASLKGLNNLAKIGLSFNSISAVDNGS
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iilarity 27.8%;
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Pred. No. 3.9e-12;
54; Mismatches 134
RPRIFKDLHFLEELQLGH
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Search completed: February 9, 2004, 11:39:05 Job time : 42 secs

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Maximum DB
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Match
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1 VEASGIGPEVPDDRDFEPSL.....QPSTFRCVYVRSAIQLGNYK 329
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  3 Q9DD03
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9 Q8NAB7
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1 Q63156
1 Q8BGT1
1 Q8BGT1
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Q9UIL7
Q8WVA2
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Q9nxp3 homo sapien
Q63156 rattus norv
Q80235 mus musculu
Q8nc95 homo sapien
Q8bgt1 mus musculu
Q75093 homo sapien
Q9uil7 homo sapien
Q9wva2 homo sapien
                                                                             Q9de03 oreochromis
Q9ddz7 petromyzon
Q9ddz8 petromyzon
Q9de00 petromyzon
Q9de04 oreochromis
Q9de04 oreochromis
Q9ddz9 petromyzon
Q8nab7 homo sapien
Q9de01 brachydanio
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45	44	43	42	41	40	39	38	37	36	35	34	ü	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
302	302.5	303.5	303.5	307	307.5	309.5	309.5	312.5	313 .	314	315	316	316.5	317	318	318.5	321.5	322	323.5	324.5	325	325	325	327	327.5	328	328.5	330
17.6	17.7	17.7	17.7	17.9	18.0	18.1	18.1	18.2	18.3	18.3	18.4	18.4	18.5	18.5	18.6	18.6	18.8	18.8	18.9	18.9	19.0	19.0	19.0	19.1	19.1	19.1	19.2	19.3
640	406	653	652	396	1346	796	376	798	1095	1025	1521	1530	1530	1525	1521	1515	376	1529	1458	1474	1523	1512	1440	1523	1531	1523	1531	120
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<b>Q9НСJ2</b>	Q8CJH0	TMBH60	Q99PH1	Q8C3D9	Q9V477	Q9WVC1	Q8BNU3	Q8WWZ2	Q90XG4	Q9Z166	095710	Q90WZ3	Q9WUG5	Q9Y5Q7	Q9R1B9	Q9DE37	Q8IV47	094813	Q8CJG8	Q8CJG9	075094	Q9DE36	Q20204	088280	088279	Q9WVB4	Q9WVB5	Q9DE02
Q9hcj2 homo sapien	Q8cjh0 rattus norv	Q9hbw1 homo sapien	Bru	Q8c3d9 mus musculu	Q9v477 drosophila	Q9wvcl rattus norv	Q8bnu3 mus musculu	Q8wwz2 homo sapien	**	Q9z166 mus musculu	O95710 homo sapien	Q90wz3 xenopus lae	Q9wug5 rattus norv	Q9y5q7 homo sapien	Q9rlb9 mus musculu	Q9de37 brachydanio	Q8iv47 homo sapien	094813 homo sapien	Q8cjg8 rattus norv	Q8cjg9 rattus norv	075094 homo sapien	Q9de36 brachydanio	Ω	O88280 rattus norv	O88279 rattus norv	Q9wvb4 mus musculu	-	Q9de02 brachydanio

## ALIGNMENTS

DRESULT 1  (OS)DE03  PRELIMINARY; PRT; 359 AA.  AC Q9DE03;  DT 01-MAR-2001 (TrEMBLrel. 16, Created)  DT 01-MAR-2003 (TrEMBLrel. 16, Last sequence update)  DT 01-MAR-2003 (TrEMBLrel. 12, Last sequence update)  DT 01-MAR-2001 (TrEMBLrel. 23, Last annotation update)  DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  DT 01-MAR-2001 (TrEMBLrel. 23, Last annotation update)  DE Corcin.  CR canthomorpha; Meanthopterygli; Peleostei; Euteleostei; Euteleostei
preliminary; prt; 359 AA.  preliminary; prt; 359 AA.  predictions (Tremblical 16, Created)  1-MAR-2001 (Tremblical 16, Last sequence update)  1-MAR-2003 (Tremblical 16, Last sequence update)  1-MAR-2003 (Tremblical 23, Last annotation update)  1-MARI; Neopterygi; Precedition update)  1-MARI; Neopterygi; Precedition update  1-MARI; Neopterygi; Prediction update  1-

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Best Local
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InterPro; IPR000372; LRR Nterm.

InterPro; IPR003591; LRR_typ.

Pfam; PF00560; LRR; 7.

Pfam; PF01462; LRRNT; 1.

SMART; SM00013; LRRNT; 1.

PROSITE; PS50506; LRR_TYPICAL; 2.

SEQUENCE 410 AA; 44671 MW; 31
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01-MAR-2001
01-MAR-2001
01-MAR-2003
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MEDLINE=20496956; PubMed=11040287;
MEDLINE10496956; PubMed=11040287;
MEDLINE10496956; PubMed=11040287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shintani S., Sato A., Toyosawa S., ("Biglycan-like extracellular matrix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Petromyzontiformes;
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                                    NNKLTRVPGGLAEHKYIQVVYLHANNISVVGSSDFCPPGHATKKASYSGVSLFSNPVQYW
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        SNVLTQVPPGLAFLKHLQVVYLHSNKLAAVKSDDFCSKGASPKRVLYSGISLFDNPVNYW
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Metazoa; Chordata; Craniata; Vertebrata;
tiformes; Petromyzontidae; Petromyzon.
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53.6%;
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; Pred. No. 2.4e-54;
51; Mismatches 90
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Pfam; PF00560; LRR; 7.
Pfam; PF01462; LRRNT; 1.
SMART; SM00013; LRRNT; 1.
PROSITE; PS50506; LRR TYPICAL; 2
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Q9DE00 PRI
Q9DE00;
01-MAR-2001 (T)
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01-MAR-2003 (T)
Biglycan-like I
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Q9DDZ8;
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01-MAR-2001
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01-MAR-2003
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"Biglycan-like extracellular matrix
J. Mol. Evol. 51:363-373 (2000).
EMBL; AF247827; AAG40162.1;
InterPro; IPR001611; LRR.
InterPro; IPR00172; LAR. Nterm.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Petromyzontiformes; Petromyzontidae; Petromyzon.
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01-MAR-2001 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
Biglycan-like protein 2
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Pfam; PF01462; LRRNT; 1.
SMART; SM00013; LRRNT; 1.
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Shintani S., Sato A., Toyosawa S., O'hUig:
"Biglycan-like extracellular matrix genes
SEQUENCE FROM N.A.

MEDLINE=20496956; PubMed=11040287;

Shintani S., Sato A., Toyosawa S., C
"Biglycan-like extracellular matrix
J. Mol. Evol. 51:363-373(2000).

EMBL; AF247821; AAG40156.1; -.
                                                                                                                                                                                              Oreochromis niloticus (Nile tilapia) (Tilapia nilotica). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroide: Cichlidae; Oreochromis.
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EMBL; AF247825; AAG40160.1; -.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Petromyzontiformes; Petromyzontidae; Petromyzon.
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    Matches
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Q9DDZ9;
01-MAR-2001
                                                                                                                 PROSITE;
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Pfam; PF01462; LRRWT; 1.
SMART; SM00013; LRRWT; 1.
PROSITE; PS50506; LRR TYPFCAL;
SEQUENCE 370 AA; 42177 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, Created
01-MAR-2001 (TrEMBLrel. 23, Last sec
01-MAR-2003 (TrEMBLrel. 23, Last an
Biglycan-like protein 1 (Fragment).
                                                                                                                                                                                                                                                                                                                                        MEDLINE=20496956; PubMed=11040287;
Shintani S., Sato A., Toyosawa S., O'hUig:
"Biglycan-like_extracellular matrix genes
                                                                                                                                                         InterPro; IPR003591; LRR
Pfam; PF00560; LRR; 8.
Pfam; PF01462; LRRNT; 1.
SMART; SM00013; LRRNT; 1.
                                                                                                                                                                                                                    InterPro; IPR001611; LRR. Lerm. InterPro; IPR000372; LRR Nterm. InterPro; IPR003591; LRR_typ.
                                                                                                                                                                                                                                                                                              J. Mol. Evol. 51:363-373 (2000).
EMBL; AF247826; AAG40161.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Petromyzontiformes; Petromyzontidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Petromyzon marinus (Sea lamprey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                               PS50506; LRR_TYPICAL;
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IPR003591;
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larity 53.0%;
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; LRR_Nterm.
; LRR_typ.
                          51.3%;
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Pred. No. 1.4e
53; Mismatches
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Score 878.5; DB 1
Pred. No. 3.4e-53;
2; Mismatches 90
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BCD0675694ECA2B7 CRC64;
                                                                                            2E07169E9BB6071B CRC64;
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                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y., Hotuta T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J., Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y., Sugiyama T., Irie R., Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "NEDO human cDNA sequencing project.";
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AK09254; BAC04007.1;
InterPro; IPR000372; LRR Nterm.
InterPro; IPR003591; LRR typ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 23, Last annotation updat
Hypothetical protein FLJ35635.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein. SEQUENCE 325 AA; 36637 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01462; LRRNT; 1.
SMART; SM00013; LRRNT; 1.
PROSITE; PS50506; LRR TYPICAL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Spleen;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8NAB7;
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64; Conservative
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                                                                                                                                                                                                                                                                                                        Score 817.5; DB 4
Pred. No. 4.6e-49;
0; Mismatches 80
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ID DEOL
  RESULT 9
Q9NXP3
ID Q9NX
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AC Q9NX
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DT 01-0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 153; Conserv
  01-OCT-2000
01-OCT-2000
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9DE01;
Q9DE01;
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50566; LRR TYPICAL;
NON TER
1 1 1
NON TER
224 224
SEQUENCE 224 AA; 24442 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. MOI. Evol. 51:363-373 (2000).

EMBL; AF247824; AAG40159.1; -.

ZFIN; ZDB-GENE-010102-1; dcn.

InterPro; IPR001611; LRR.
                                                                            Q9NXP3
                                                                                                   Q9NXP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003591; LRR_typ. Pfam; PF00560; LRR; 7. SMART; SM00369; LRR_TYP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shintani S., Sato A., Toyosawa S., ("Biglycan-like extracellular matrix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20496956; PubMed=11040287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         296
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224 AA;
  (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
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                                                                                                      PRELIMINARY;
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23,
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16,
23,
Created)
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Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniform
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                        YLSKNOLKELPEKMPKTLOELRAHENEITKVRKVTFNGLNOMIVIELGTNPLKSSGIENG
||||| |||:| :||:||| |||:||:||:||
YLSKNLLKEVPANIPKSLOELRIHENQINKIKKSSFAGKANVIVMELGSNPLSSSGVDNG
                                                                                                                                                                                                                                                                                      VPKDLPPDTTLLDLQNNKITEIKDGDFKNLKNLHALILVNNXISKVSPGAFTPLVKLERL
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                         NSISAVDNGSLANTPHLRELHLDNNKLTRVPGGLAEHKYIQV
                                                                                                          AFQGMXKLSYIRIADTNITSIFQGLFBSLTELHLDGNKISRVDAASLKGLNNLAKLGLSF
                                                                                                                                                                                                                                                               VPEKIPLDTTLLDLQNNKITEIKENDFKGLKGLQTLILVNNKITIIHAKAFSSLINLERL
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NEISVVENGSLANVPHLRELHLENNALTAVPAGLADHKY I QV
                                                                                     AFADLKRVSAIRIADTNLTSIPKGLPSSLFELHLDGNKITKVTADSLKGLKNLSKLGLSH
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                                                                                                                                                                                                                                                                                                                                                  45.8%; Score 784; DB 13;
68.9%; Pred. No. 6.1e-47;
tive 30; Mismatches 39
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Last annotation updat
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                                         266
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Q6315
Q6315
AC Q6315
AC Q6315
DF 01-W
DF RAMMA
OC RAMMA
OC NCBI
RA NGBI
RA MOSE
RT "EXP
TRAI
RA MOSE
RT Inju
RT SUBJ
RF EMBL/
DR Intes
DR Intes
DR Intes
DR Pfam,
DR Pfam,
DR PROSJ
PT NON 7
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  Query Match
Best Local S
Matches 96
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Matches
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                                                                                              PROSITE;
NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                      (1)
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=Sprague-Dawley; TISSUE=Lung;
Woats-Staats B.M., Stiles A.D., Xu
Moats-Staats B.M., Stiles A.D., Xu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q63156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y. Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Sh. Tanaka T., Nakamura Y., Isogai T., Sugano S.;
"NEDO human cDNA sequencing project.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AKO00136; BAA90967.1; -.
InterPro; IPR00151; LRR.
InterPro; IPR003991; LRR.
InterPro; IPR003991; LRR.
IPFam; PF00560; LRR; J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Decorin (Fragment).
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical
                                                                                                                                                                                                      EMBL; L75825; ARAB5371.1; --
EMBL; L75825; RARAB5371.1; --
InterPro; IPR001611; LRR.
InterPro; IPR003591; LRR_typ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                      Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                               PF00560; LRR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           μ
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                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PS50506; LRR_TYPICAL; ical protein.
187 AA; 21074 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LNQMIVIELGTNPLKSSGIENGAPQGMKKLSYIRIADTNITSIPQGLPPSLTELHLDGNK
                                                                                                                                                                 00560; LRR; 3.
PS50506; LRR TYPICAL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VOLGNE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ISRVDAASLKGLNNLAKLGLSFNSISAVDNGSLANTPHLRELHLDNNKLTRVPGGLAEHK
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                                                                                                96
28.4%; ilarity 100.0%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                              96
6 AA;
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                                                                                                10398 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23,
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Last sequence update)
Last annotation updat
    0
                      Score 487;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 548.5; DB 4;
Pred. No. 1.1e-30;
2; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                C6D19F1750B050D0 CRC64;
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Best Local S
Matches 93
                                                                                                                                                             Q8NC95 PRELIMINARY; PR
Q8NC95;
O1-CCT-2002 (TrEMBLrel. 22, Crea
O1-CCT-2002 (TrEMBLrel. 22, Last
O1-MAR-2003 (TrEMBLrel. 23, Last
Hypothetical protein FLJ90402.
Homo sapiens (Human)
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the RIKEN Genome Exploration Research Group Phase I & II
"Analysis of the mouse transcriptome based on functional
60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
EMBL; AK037150; BAC29722.1;
SEQUENCE 378 AA; 43293 MW; 6F85AlB935FFFB8C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2003 (TYENHBLrel. 23, Created)
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01-MAR-2003 (TYENHBLrel. 23, Last annote
proline arginine-rich end leucine-rich
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                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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01-MAR-2003
SEQUENCE FROM N.A.
                                                    NCBI_TaxID=9606;
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nilarity 32.2%;
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                                                                                                     Chordata;
Primates;
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Pred. No. 6e-19;
57; Mismatches 1:
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Catarrhini;
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annotation update)
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Pfam; PF00560; LRR; 1.
Pfam; PF01463; LRRCT; 1.
Pfam; PF01462; LRRUT; 1.
SMART; SM00002; LRRUT; 1.
SMART; SM00013; LRRUT; 1.
PROSITE; PS50506; LRR TYPICAL; 1
PROSITE; PS00119; PA2_ASP; 1.
                                                                                                                                                                                                                                                                                            Q8BGT1;
Q8BGT1;
01-MAR-2003
01-MAR-2003
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   The FANTOM Consortium,
the RIKEN Genome Exploration Research Group
"Analysis of the mouse transcriptome based
60,770 full-length cDNAs.";
Nature 420:563-573(2002)
EMBL; AK028252; BAC25843.1; -.
EMBL; AK031464; BAC27417.1; -.
                                                                                                                       SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Head, and Testis;
MEDLINE=22354683; PubMed=12466851;
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InterPro; IPR001611; LRR.
InterPro; IPR001631; LRR. Cterm.
InterPro; IPR000372; LRR. Nterm.
InterPro; IPR003591; LRR. Typ.
InterPro; IPR003591; LRR. Typ.
InterPro; IPR001211; PhospholipaseA2.
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01-MAR-2003 (TrEMBLrel. 2
01-MAR-2003 (TrEMBLrel. 2
Fibronectin leucine rich
                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                            Mus musculus (Mouse).
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Rodentia;
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th transmembrane protein 3 homolog.
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Pred. No. 1
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Sciurognathi;
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based on func
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thi; Muridae; Murinae; Mus
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functional
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     PRINTS;
SMART; S
SMART; S
SMART; S
SMART; S
                                                                                                                                                                  Pfam;
Pfam;
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EMBL; AB017167; BAA35184.1; -.
HSSP; P00743; 1CCF.
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01-AUG-1999 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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Itoh A., Miyabayashi T., Ohno M., Sakano
"Cloning and expressions of three mammali
slit suggest possible roles for slit in t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Slit-1 protein.
                                                                                                                                                 Pfam;
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                                                                                                                                                                                                      InterPro;
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PF01463; LRRCT; 4.

PF01462; LRRNT; 4.

PF01462; LRRNT; 4.

SPF00011; EGFLAMININ.

SM00041; CT; 1.

SM00019; EGF CA; 2.

F; SM00274; FOLN; 3.

F; SM00274; FOLN; 3.

F; SM00282; LRRCT; 4.
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IPR003645;
IPR002049;
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IPR001881; 1
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IPR006207; Cys knot C.
IPR000742; EGF Z.
IPR001881; EGF Ca.
IPR006209; EGF like.
IPR003645; FolN.
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                                                                                                                                                 LRR; 19
                                                                                                                                                                                       EGF; 9.
                                                                                                                                                                laminin_G; 1.
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Laminin_G.
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11,
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Pred. No. 1.5e-15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lian
the
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QUULT 15
QUULT 16
QUULT 17
ID QUUIT 20
QUUIT 01-MA
DT 01-MA
DT 01-MA
DT 01-MA
ON MEGF4
GN MEGF4
GN MEGF4
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GN MEDLI
RN I1]
RN I1]
RN I1den
RT 11kee
DR HSSP;
DR HSSP;
DR HSSP;
DR Intex
DR Intex
DR Intex
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                              MEDLINE-98360089; PubMed-9693030;
Nakayama M., Nakajima D., Nagase T., Nomura
"Identification of high-molecular-weight pr
like motifs by motif-trap screening.";
Genomics 51:27-34(1998).
EMBL; AB011537; BA32465.3; -.
HSSP; P00743; ICCP.
Genew; HGNC:11085; SLITI.
                                                                                                                                                                                                                              OSUIL7;
OSUIL7;
01-MAY-2000 (TREMBLrel. 1
01-OCT-2002 (TREMBLrel. 2
01-MAR-2003 (TREMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SN
SMART; SN
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
            InterPro;
InterPro;
                                                                                                                              SEQUENCE FROM N.A.
TISSUE=Brain;
                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                        Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                       MEGF4 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; SM00013; LRENT; 4.
; SM00369; LRR TYP; 10.
TE; PS00010; AST HYDROXYL; 2
TE; PS01185; CTCK 1; 1.
TE; PS01225; CTCK 2; 1.
TE; PS01225; EGF 1; 9.
TE; PS01186; EGF 2; 8.
TE; PS01187; EGF CA; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 VPDDRDF----BPSLGPVCPFRCQCHLRVVQCSDLGLDKVPKDLPPDTTLLDLQNNKITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                  QCPQECACLDTVVRCSNKHLRALPKGIPKNVTELYLDGNQFTLV-PGQLSTFKYLQLVDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             domain
                                                                                                                                                                                                                                                                                                                                                                                   SNNKISSISNSSFTNMSQLTTLILSYNALQCIPPLAFQGL---RSLRLLSLHGNDISTLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                             EGIF----ADVTSLSHLAIGANPL
                                                                                                                                                                                                                                                                                                                                                            SSDFCPPGHNTKKASYSGVSLFSNPV
                                                                                                                                                                                                                                                                                                                                                                                                          SFNSISAVDNGSLANTPHLRELHLDNNKLTRVP----GGLAEHKYIQVVYLHNNNISVVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FNCNCQLAWLGGWLRKRKIVTGNPRCQNPDFLRQIPLQDVAFPDFRCEEGQEEGGCLPRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LRTLMLRNNRISCIHNDSFTGLRNVRLLSLYDNQITT--VSPGAFDTLQSLSTLNLLANP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LRA---HENEITKVRKVTFNGLNOMIVIELGTNPLKSSGIENGAFOGMKKLS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEATGMFKKLTHLKKINLSNNKVSEIEDGAFEGAASVSELHLTANQLESIRSGMFRGLDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IK-DGDFKNLKNLHALILVNNKISKVSPGAFTPLVKLERLYLSKNQLKELPEKMPKTLQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPGTEDYQLNSECNSDVVCPHKCRCEANVVECSSLKLTKIPERIPQSTAELRLNNNEISI
IPR000152; Asx_hydroxyl.
IPR006207; Cys_knot_C.
IPR000742; EGF_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1534 AA; 167952 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                       Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19.5%;
                                                                                                                                                                                                                                22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 334.5; DB 4; ; Pred. No. 1.3e-14; 65; Mismatches 121;
                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                               PRT;
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                                                                                          Nomura N., Seki N., Ohara (
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EGF-
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                                  RESULT 16
Q8WVA2
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Best Local S
Matches 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00010; ASX HYDROXYL; 2
PROSITE; PS01185; CTCK 1; 1.
PROSITE; PS01255; CTCK 2; 1.
PROSITE; PS00022; EGF 1; 9.
PROSITE; PS01186; EGF 2; 8.
PROSITE; PS01187; EGF 2; 8.
PROSITE; PS01187; EGF 2; 8.
PROSITE; PS0025; LAM G DOMAIN; 1
PROSITE; PS50026; LRR_TYPICAL; 5.
 Q8WVA2;
Q8WVA2;
01-MAR-2002
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Pfam;
Pfam;
Pfam;
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EGF-like
NON_TER
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SMART;
SMART;
SMART;
SMART;
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InterPro;
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Pfam; PF01462; LRRNT; 4.
PRINTS; PR00010; EGFBLOOD.
PRINTS; PR00019; LEURICHRPT.
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SW00181; EGF; 9.

SW00179; EGF CA; 9.

SW00282; LamG; 1.

SW00082; LRRCT; 4.

SW00013; LRRNT; 4.
                                                                                933
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PF00054; lamir
                                                                                                                                                                                                                                                                                                                                       66
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                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
97; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SM00369;
                                                                                                                                                                                                                                                                                                                                                                                   VPDDRDF----EPSLGPVCPFRCQCHLRVVQCSDLGLDKVPKDLPPDTTLLDLQNNKITE
                                                                                                                                                                       domain.
                                                                                                                                                                                                                                                                                                                 LEATGMFKKLTHLKKINLSNNKVSEIEDGAFEGAASVSELHLTANQLESIRSGMFRGLDG
                                                                                             SSDFCPPGHNTKKASYSGVSLFSNPV 304
                                                                                                                           SNNKISSLSNSSFTNMSQLTTLILSYNALQCIPPLAFQGL---RSLRLLSLHGNDISTLQ
                                                                                                                                                  SENSISAVDNGSLANTPHLRELHLDNNKLTRVP----GGLAEHKYIQVVYLHNNNISVVG
                                                                                                                                                                                                                                                                                        LRA---HENEITKVRKVTFNGLNOMIVIELGTNPLKSSGIENGAFQGMKKLS------
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                                                                                                                                                                                                                                                                                                                                                             I PGTEDYQLNSECNSDVVCPHKCRCEANVVECSSLKLTKI PERI PQSTABLRLNNNEISI
                                                                                EGIF----
                                                                                                                                                                                                                      FNCNCQLAWLGGWLRKRKI VTGNPRCQNPDFLRQI PLQDVAFPDFRCEEGQEEGGCLPRP
                                                                                                                                                                                                                                                                  LRTLMLRNNRISCIHNDSFTGLRNVRLLSLYDNQITT--VSPGAFDTLQSLSTLNLLANP
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IPR001611;
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  (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                        PRELIMINARY;
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                                                                                -ADVTSLSHLAIGANPL
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LRR_Nterm.
LRR_typ.
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EGF_II.
EGF_like.
IEGF.
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  20,
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Pred. No. 1.4e-14;
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                         674
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1618; 103;

Gaps

638

65

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869

816

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RESULT
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Best Local S
Matches 88
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Pfam; PF00560; LRR; 8.
Pfam; PF001463; LRRCT; 1.
Pfam; PF01462; LRRNT; 1.
SMART; SM00080; FN3; 1.
SMART; SM00081; LRRCT; 1.
SMART; SM00081; LRRCT; 1.
SMART; SM00089; LRR TYP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Che
Mammalia; Eutheria; Pri
                                                                         Q9DE02;
Q9DE02;
01-MAR-2001
Brachydanio rerio (Zebrafish)
Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii;
                                         01-MAR-2001 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
Biglycan-like protein 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical SEQUENCE 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ
EMBL; BC010370; AAH18370.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003961; FN_III.
InterPro; IPR001611; LRR.
InterPro; IPR001483; LRR_Cterm.
InterPro; IPR000372; LRR_Nterm.
InterPro; IPR003591; LRR_typ.
InterPro; IPR001211; PhospholipaseA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                   OR BGL3.
                                                                                                                                                   324
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                                                                                                                                                                                                                                                                                                                                                                                                         88;
                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PS50506; LRR TYPICAL;
PS00119; PA2 ASP; 1.
                                                                                                                                                                                                                                                                                                                                                                                    CPFRCQCHLRVVQCSDLGLDKVPKDLPPDTTLLDLQNNKITEIKDGDFKNLKNLHALILV
                                                                                                                                                                      SLFSNP
                                                                                                                                                                                                                                 NOMIVIELGTNPLKSSGIENGAFOGMKKLSYIRIADTNITSIPQGLPPSLTELHLDGNKI
                                                                                                                                                                                                                                                                                                                               NNKISKVSPGAFTPLVKLERLYLSKNQLKELPEKMPKTLQELRAHENEITKVRKVTFNGL
                                                                                                                                                                                                                                                                                                                                                               CPSVCRCDNGFIYCNDRGLTSIPADIPDDATTLYLQNNQINNA--GIPQDLKT----
                                                                                                                                                                                           AHLQKLYLQDNAISHIPYNTLAKMRELERLDLSNNNLTTL----
                                                                                                                                                                                                                                                       SRVDAASLKGLNNLAKLGLSFN
                                                                                                                                                                                                                                                                           PLLEKLHLDDNSVSTVSIEEDAFADSKQLKLLFLSRNHLSSIPSGLPHTLEELRLDDNRI
                                                                                                                                                                                                               -HLRELHLDNNKLTRVP-GGLAEHKYIQVVYLHNNNISVVGSSDFCPPGHNTKKASYSGV
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                                                                        (TrEMBLrel.
                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
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Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  74087 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                   19.4%;
                                          . 16, Created)
. 16, Last sec
. 23, Last and
3 (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                         59;
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Last
                                                     Last sequence up
  n) (Danio rerio)
h; Craniata; Veri
; Teleostei; Osta
                                                                                                                                                                                                                                                                                                                                                                                                                     Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                              Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Eutele Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  38AB53F7243166CC
                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence update)
annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                    332;
No. 6
                                                                                              120
                                                                                                                                                                                                                                                                                                                                                                                                                     <u>ه</u>
Vertebrata; Eu
                                                                                                                                                                                                                                                                                                                                                                                                                              DB
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                                                    on update)
                                                                                                                                                                                                                                                                                                                                                                                                         103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                         Indels
            Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Euteleostomi;
  Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                              674;
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RESULT 18
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Best Local S
Matches 63
           Pfam; PF00008;
Pfam; PF00560;
Pfam; PF01463;
Pfam; PF01462;
SMART; SM00041;
                                                                                                                                                                                                                                                                                                                                    01-NOV-1999
01-NOV-1999
01-MAR-2003
SLIT1.
SLIT1.
                                                                                                                                                                                                            STRAIN-Swiss Webster/ICR;

MEDLINE=99365246; PubMed=10433822;

Yuan W., Zhou L., Chen J.H., Wu J.Y., Rao Y.,

"The mouse 'SLIT family: secreted ligands for R

patterns that suggest a role in morphogenesis

Dev. Biol. 212:390-306(1999).
                                                                                                                                                                                                                                                                                                                                                                                     Q9WVB5
                                                                                                                                InterPro;
InterPro;
                                                                                                                                                                                 HSSP;
                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON_TER
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EMBL; AF247823; AAG40158.1; -.
ZFIN; ZDB-GENE-010131-5; bgl3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00560; LRR; 4.
PROSITE; PS50506; LRR_TYPICAL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shintani S., Sato A., Toyosawa S., (
"Biglycan-like extracellular matrix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=20496956; PubMed=11040287;
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001611; LRR.
InterPro; IPR003591; LRR_typ:
Pfam; PF00560; LRR; 4.
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NCBI_TaxID=7955;
                                                                                 [nterPro;
                                                                                           [nterPro;
                                                                                                    [nterPro;
                                                                                                                       InterPro;
                                                                                                                                                   InterPro;
                                                                                                                                                              InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63;
                                                                                       j IPR000152; Asx hydroxyl.
j IPR006207; Cyg knot_C.
j IPR000742; EGF_Ca.
j IPR001881; EGF_Ca.
j IPR003649; EGF_like.
j IPR003645; FolN.
j IPR001611; LRR.
j IPR001631; LRR. Cterm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KVPKOLPPDTTLLDLQNNKITEIKDGDFKNLKNLHALILVNNKISKVSPGAFTPLVKLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                           LYLSKNOLKELPEKMPKTLQELRÄHENEITKVRKVTFNGLNOMIVIELGTNPLKSSGIE
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120 AA;
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LRRCT; 4.
LRRNT; 4.
; CT; 1.
; EGF_CA; 2.
                                         laminin_G; 1.
LRR; 19.
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                                                                             LRR_Oterm.
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                                                                  LRR_typ
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12,
23,
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                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                           Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        330;
No. 9.
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.8e-16;
                                                                                                                                                                                                                                   for ROBO
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                                                                                                                                                                                                                        axon
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DR RC STAR RC 
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Best Local S
Matches 94
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SMART; SM
SMART; SM
SMART; SM
SMART; SM
SMART; SM
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                       Q9WVB4;
Q9WVB4;
01-NOV-1999
01-NOV-1999
01-MAR-2003
SEQUENCE FROM N.A.
STRAIN-Swiss Webster/ICR;
MEDLINE=99365246; PubMed=10433822;
MEDLINE=99365246; PubMed=10433822;
Yuan W., Zhou L., Chen J.H., Wu J.Y., Rao Y., Ornitz
"The mouse SLIT family: secreted ligands for ROBO exp
patterns that suggest a role in morphogenesis and axo
Dev. Biol. 212:290-306(1999).
EMBL; AF144629; AAD44760.1; -.
HSSP; P01132; 1EGF.
MGD; MGI:1315202; Slit3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                        Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                      19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; SM00274; FOLN; 2.
; SM00282; LARG; 1.
; SM00082; LRRCT; 4.
; SM00013; LRRNT; 4.
; SM00369; LRR_TYP; 10.
                                                                                                                                                                                                                                                                                                                                                                                                                      852
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                                                                                                                                                                                                                                                        (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; PS00010; ASX HYDROXYL; 2.
3; PS01185; CTCK 1; 1.
3; PS01225; CTCK 2; 1.
4; PS0022; EGF 1; 9.
5; PS01186; EGF 2; 8.
6; PS01186; EGF 2; 8.
6; PS01187; EGF CA; 2.
6; PS0186; LAM G DOMAIN; 1.
6; PS50025; LAM G DOMAIN; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    FCPPGHNTKKASYSGVSLFSNPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FNCNCHLSWLGDWLRKRKIVTGNPRCQNPDFLRQIPLQDVAFPDFRCEEGQEEVGCLPRP
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                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                    -ADVTSLSHLAIGANPL
                                                                                                                                                                                          Chordata;
Rodentia;
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12,
23,
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                                                                                                                                                                                                                                                                       Created)
Last sequence
Last annotation
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Pred. No. 3.3e-14;
"" matches 127;
                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                       sequence update) annotation updat
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                                                           itz D.M.;
expressed in
axon guidance.";
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Best Local S
Matches 99
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SMART; SM00041; CT; 1.
SMART; SM00179; BGF CA; 1.
SMART; SM00282; LAMG; 1.
SMART; SM00082; LARCT; 4.
SMART; SM00013; LARNT; 4.
SMART; SM00013; LARNT; 4.
SMART; SM00013; LARNT; 4.
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PRINTS;
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PROSITE;
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EGF-like
NON TER
SEQUENCE
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Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 interPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nterPro;
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                  20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF00054;
                                                                385 LLNANKINCLRVNTF---
                                                                                                                                                            209
                                                                                                                                                                                            265
                                                                                                                                                                                                                           183
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                                                                                                                                                                                                                                                                                                                                                                                                                    78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; P$00010; ASK HYDROXYL; 2

3; P$01185; CTCK 1; 1.

3; P$01225; CTCK 2; 1.

3; P$01022; EGF 1; 9.

3; P$01186; EGF 2; 7.

5; P$01187; EGF C1; 1.

5; P$50025; LAM G DOMAIN; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PR00010; EGFBLOOD.
PR00011; EGFLAMININ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              # domain.
1523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS501187;
PS50025;
PS50506;
                                                                                                                                                                                                                                                                                                                                              KVRKVTFNGLNQMIVIBLGTNPLKSSGIENGAPQGMKKLSYIRIADTNI-------
                                                                                                                                                                                                                                                                                                                                                                                     RVLHLEDNOVSIIERGAFODLKQLERLRLNKNKLOVLPELLFOSTPK-LTRLDLSENQIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GP---VCPFRCQCHLRVVQCSDLGLDKVPKDLPPDTTLLDLQNNKITEIKDGDFKNLKNL
                                                                                                                                                                                                                                                                                                                                                                                                                   HALILVNNKISKVSPGAFTPLVKLERLYLSKNOLKELPEKM----PKTLQELRAHENEIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                  YLHNNNISVVGSSDFCPPGHNTKKASYSGVSLFSNPVQ
                                                                                                                            GAFTQYKKLKRIDISKNQISDIAPDAFQGLKSLTSLVLYGNKITEIPKGLFDGLVSLQLL
                                                                                                                                                                                        GPHSEAPACNANSLSCPSACSCSNNIVDCRGKGLTEIPANLPEGIVEIRLEQNSIKSIPA
                                                                                                                                                                                                                                                                                                                     GIPRKAFRGVTGVKNLQLDNNHI--SCIEDGAFRALRDLEILTLNNNNISRILVTSFNHM
                                                                                                                                                         ASLKGLNNLAKLGLSFNSISAVDNGSLANTPHLRELHLDNNKLTRVPGGLAEHKY-IQVV
                                                                                                                                                                                                                                                        PKIRTLRLHSNHLYCDCHLAWLSDWLRQRRTIGQFTLCMAPVHLRGFSVADVQKKEYVCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR003591;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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LRRNT; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      laminin_G; 1.
LRR; 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAM_G DOMAIN LRR_TYPICAL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Asx_hydroxyl.; Cys_knot_C.
EGF_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LRR. Cterm.
LRR_Nterm.
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EGF_Ca.
EGF_II.
EGF_like.
Laminin_EGF.
Laminin_G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 167711 MW; F43A3F3E016C4BFC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LRR_typ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 328; DB
Pred. No. 3.5e-
53; Mismatches
                                                                ---QDLQNLNLLSLYDNKLQ
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                                                                                                                                                                                                                           ----TSIPQGLPPSLTELHLDGNKISRVDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124;
                                                                416
                                                                                                305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
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Gaps

146 133 87 77

204 182

324 208 264 182

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Best Local S
Matches 96
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SMART; S'
SMART; S'
SMART; S'
SMART;
SMART;
SMART;
                                                                                                                                                                                                                                                                                                                           SMART; SM00369; LRR_TYP; 10.

PROSITE; PS00010; ASX HYDROXYL; 2.

PROSITE; PS01185; CTCK 1; 1.

PROSITE; PS01255; CTCK 2; 1.

PROSITE; PS0022; EGF 1; 9.

PROSITE; PS01186; EGF 2; 8.

PROSITE; PS01187; EGF CA; 2.

PROSITE; PS0155; LAM G DOMAIN; 1.

PROSITE; PS05056; LRR_TYPICAL; 5.

EGF-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         088279;
088279;
01-NOV-1998
01-NOV-1998
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam;
Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam;
Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Sprague-Dawley; TISSUE-Brain; MEDLINE=9836089; PubMed=9693030; Nakayama M., Nakajima D., Nagase T., Nomura "Identification of high-molecular-weight prolike motifs by motif-trap screening."; Genomics 51:27-34(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
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InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AB011530; BAA32460.1; -. HSSP; P00743; 1APO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ); PF00560; LRR; 19.

; PF01463; LRRUT; 4.

; PF01463; LRRUT; 4.

TIS; PR00011; EGFLAMINI
TI; SM00149; CT; 1.

TI; SM00179; EGF CA; 2.

TI; SM00274; F0LN; 3.
      615
                                                                              555
                                        125
                                                                                                                                                      495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PF00008; EGF;
PF00054; lami
                                                                                                                  66
                                                                                                                                                                                              10
                                                                                                                                                                                                                                  96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SM00082;
                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; IPR000152; Asx hydroxyl.; IPR006207; Cys knot_C.; IPR000742; EGF_2.; IPR0001881; EGF_Ca.; IPR003645; FOLN.
                                                                                                                                                                    VPDDRDF----EPSLGPVCPFRCQCHLRVVQCSDLGLDKVPKDLPDDTTLLDLQNNKITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; IPR003645;
; IPR002049;
; IPR001791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; IPR006207;
; IPR000742;
; IPR001881;
                                                                                          IK-DGDFKNLKNLHALILVNNKISKVSPGAFTPLVKLERLYLSKNOLKELPEKMPKTIQE 124
                                    LRA---HENEITKVRKVTFNGLNOMIVIELGTNPLKSSGIENGAFQGMKKLS-----
                                                                      LEATGLFKKLSHLKKINLSNNKVSEIEDGTFEGATSVSELHLTANQLESVRSGMFRGLDG
                                                                                                                                                  IPGTEDYHLNSECTSDVACPHKCRCEASVVECSGLKLSKIPERIPQSTTELRLNNNEISI
LRTLMLRNNR ISCIHNDSFTGLRNVRLLSLYDNHITT---ISPGAFDTLQALSTLNLLANP
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                                                                                                                                                                                                                              19.1%;
ilarity 24.9%;
Conservative 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; EGFLAMININ.; CT; 1.; EGF CA; 2.; FOLN; 3.; Lamg; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LRRCT; 4.
LRRNT; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      minin_G; 1.
                                                                                                                                                                                                                                                                                                           167497 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Laminin_EGF
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08,
23,
                                                                                                                                                                                                                                65;
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Last sequence up
Last annotation
                                                                                                                                                                                                                          Score 327.5; DB 11;
Pred. No. 3.9e-14;
5; Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                               5
                                                                                                                                                                                                                                                                                                         DFC4B60CCBC5529A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1531
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ns with m
                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ., Ohara O
                                                                                                                                                                                                                            103;
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672
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DA CON CONTRACTOR CONT
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                                                                                                                                                                                                  Pfam; PF01463; LRRCT; 4.
Pfam; PF01462; LRRNT; 4.
Pfam; PF01462; LRRNT; 4.
PRINTS; PR00010; EGFLAMINI
PRINTS; PR00011; EGFLAMINI
PRINTS; PR00019; LEURICHRP
SMART; SM00041; CT; 1.
SMART; SM00074; CT; 1.
SMART; SM00082; LARGT; 1.
SMART; SM00082; LRRCT; 4.
SMART; SM00082; LRRCT; 4.
SMART; SM00082; LRRCT; 4.
SMART; SM00083; LRRCT; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000152; Asx hydroxyl.
InterPro; IPR006207; Cyg knot C.
InterPro; IPR00742; EgF 2.
InterPro; IPR001881; EGF 2.
InterPro; IPR001438; EGF II.
InterPro; IPR001438; EGF III.
InterPro; IPR001439; EgF-like.
InterPro; IPR002049; Laminin EGF.
InterPro; IPR001791; Laminin G.
InterPro; IPR001791; Laminin G.
InterPro; IPR000483; LRR Cterm.
InterPro; IPR000372; LRR_Nterm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O88280;
O88280;
O1-NOV-1998
O1-NOV-1998
O1-MAR-2003
                                         PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
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Pfam;
Pfam;
Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AB011531; BAJ
HSSP; P01132; 1EGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomics 51:27-34(1998)
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"ART; SM00041; CT; 1.

"WART; SM00041; CT; 1.

"WART; SM00179; EGF CA; 1.

"ART; SM00179; EGF CA; 1.

"AT; SM000182; LAMG; 1.

"T; SM000369; LAR TYP; 9.

"T; SM00369; LAR TYP; 9.

"T; PS001185; CTCK 1; 1.

"E; PS01125; CTCK 2; 1.

"E; PS01186; EGF 2; 7.

"PS011186; EGF CA; 2.

"PS011187; EGF CA; 2.

"PS011187; EGF CA; 2.

"PS011187; EGF CA; 2.

"PS01187; EGF CA; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PF00008; EGF; 9.
PF00054; laminin_G; 1.
PF00560; LRR; 19.
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Last sequence update)
Last annotation update)
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Sciurognathi; Muridae;
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EGF-
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Best Local (
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Q20204;
Q1-NOV-1996
Q1-MAY-2000
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EGF-like
SEQUENCE
                                SEQUENCE FROM N.A.

Sumye R.;

Submitted (MAR-1998) to the EMBL/GenBank/DDBJ

EMBL; Z69792; CAA93668.2; -.

EMBL; AL022270; CAA93668.2; JOINED.

EMBL; AL022270; CAA93434.1; -.

EMBL; Z69792; CAB63434.1; JOINED.

HSSP; P00740; IEDM.
                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
                                                                                                                                   investigating biology.";
Science 282:2012-2018(1998).
                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                             F40E10.4 protein.
                                                                                                                                                                                                                                                                                                                            01-MAR-2003
WormPep; F40E10.4; CE23711.
InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR006207; Cys_knot_C.
                                                                                                                                                "Genome sequence of the nematode investigating biology.";
                                                                                                                                                                    none;
                                                                                                                                                                                                               Submitted
                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                         Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RVLHLEDNQVSVIERGAFQDLKQLERLRLNKNKLQVLPELLFQSTPK-LTRLDLSENQIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HALILVNNKISKVSPGAFTPLVKLERLYLSKNOLKELPEKM----PKTLQELRAHENEIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GP----VCPFRCQCHLRVVQCSDLGLDKVPKDLPPDTTTLDLQNNKITEIKDGDFKNLKNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAFIQYKKLKRIDISKNQISDIAPDAFQGLKSLTSLVLYGNKITEIPKGLFDGLVSLQLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GIPRKAFRGVTGVKNLQLDNNHI--SCIEDGAFRALRDLEILTLNNNNISRILVTSFNHM
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                                                                                                                                                                                                                                                                                                                                                                                                                           LLNANKINCLRVNTF---
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0 (TrEMBLrel.
3 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                Nematoda;
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Last seq
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                                                                                                                                                                                                              EMBL/GenBank/DDBJ
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annotation update)
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                                                                                                                                                       platform
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  RESULT 23
Q9DE36
ID Q9DE3
AC Q9DE3
DT 01-MA
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Best Local Sin
Matches 107;
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PRINTS; PRO0010; LEURICHRPT.
SMART; SM00041; CT; 1.
SMART; SM000179; EGF CA; 2.
SMART; SM00082; LERGT; 1.
SMART; SM00082; LERGT; 4.
SMART; SM00013; LERNT; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS0001; ASX HYDROXYL; 1
PROSITE; PS01225; CTCK 2; 1.
PROSITE; PS01225; CTCK 2; 1.
PROSITE; PS01186; EGF 2; 5.
PROSITE; PS01187; EGF CA; 1.
PROSITE; PS50025; LAM G DOMAIN; 1
PROSITE; PS50566; LRR TYPICAL; 4.
  Q9DE36;
Q9DE36;
01-MAR-2001
01-MAR-2001
01-MAR-2003
Slit2.
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EGF-like
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Pfam;
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Pfam;
Pfam;
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InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                NNKISKVSPGAFTPLVKLERLYLSKNQLKELPEKM-----
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                                                                                                                                                                                                TABICPLPCTCTGTTVDCRDSGLTYVPTNLPPSTTEIRLEQNQISSIPSHSFKNLKNLTR
                                                                                                                                                                                                                                                                                                             --PKTLQELRAHENEI-----TKVRKVTFNGLNQMIVIE--
                                                                                                            CIRRGTFDHVP-----KLSMLSLYDNDIK--SISEVTFQNLTSLSTLHL
                                                                                                                                VV--GSSDFCPPGHNTKKASYSGVSLFSNPVQYWEIQPSTFRCVYVRSAIQL
                                                                                                                                                       LDLSKNIITEIQPKAFLGLHNLHTLYLYGNNITDLKSDTFEGLGS----LQLLLLNANQLT
                                                                                                                                                                           LGLSFNSISAVDNGSLANTPHLRELHLDNNKLTRVPG----GLAEHKYIQVVYLHNNNIS
                                                                                                                                                                                                                                             PWNCDCRLRWMRKWLEKAEGQNKTVCATPLNLQGSSIEILQDKFMTCSGNRKRRYKKTCE
                                                                                                                                                                                                                                                                 P-----QGMKKLSY----
                                                                                                                                                                                                                                                                                       QGPBFLEVLNLDKNHIFCLENNVISSWVSLEVLTLNG-NRLTTFEEPSNARFRQLDLFNN
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           (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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LRR; 18.
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; LRR_Cterm.
; LRR_Nterm.
; LRR_typ.
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M G DOMAIN; )
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EGF_Ca.
EGF_II.
EGF_like.
EGF_lin_G.
            23,
                                                                                                                                                                                                                                                                                                                                                                                                                        62;
           Created)
Last sequence up
Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 325; DB
Pred. No. 5.3e-
62; Mismatches
                                                      PRT;
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:.3e-14;
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                      update)
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            update)
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136 118 76 83 Gaps

13;

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Best Local S
Matches 98
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PRINTS;
SMART; S
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SEQUENCE
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PROSITE;
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                                                                                                                                                                                                                                  SMART;
                                                                                                                                                                                                                                                SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brachydanio rerio (Zebrafish)
Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii; T
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                      Pfam;
Pfam;
                                                                                                                                                                                                                                                              SMART;
                                                                                                                                                                                                                                                                                        Pfam;
                                                                                                                                                                                                                                                                                                                  Pfam; PF0000
                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-Michigan
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                            ZFIN; ZDB-GENE-010306-3; slit2.
                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P00740; 1EDM
                                                                                                                                                                                                                                                                                                                            interPro;
                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                            nterPro;
                                                                                                                                                                                                                                                                                                                                                                                        interPro;
                                                                                                                                                                                                                                                                                                                                                                                                interPro;
                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                Zebrafish slit2 homolog.";
hubmitted (DEC-1999) to the
                                                                                                                                                                                                                                                                                                                                                nterPro;
                                                                                                                                                                                                                                                                                                                                                     nterPro;
                                                                                                                                                                                                                                                                                                                                                                           nterPro;
                                                                                                                                                                                                                                                                                                                                                                                  nterPro;
                                                                                                                                                                                                                                                                                                                                                                    nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                               eo S.Y.,
  183
               199
                             183
                                         141
                                                        141
                                                                                                                                                                                                                                                                                                      PF00054;
                                                                                                                                                                                                                          ; SM00041; CT; 1.
; SM00179; EGF CA; 2.
; SM00274; FOLN; 2.
; SM00282; LAMG; 1.
; SM00082; LRRCT; 4.
; SM00013; LRRUT; 4.
; SM00013; LRRUT; 4.
                                                                     81
                                                                                  84
                                                                                                                                                                                                                                                                                         PF01462;
                                                                                                21
                                                                                                             24
                                                                                                                           l Similarity
98; Conserv
                                                                                                                                                      domain.
                                                                                                                                                                  PS50025;
PS50506;
                                                                                                                                                                                                              PS00010;
                                                                                                          RGSTEIKNLQLDYNQI--SCIEDGAFRALGDLEVLTLNNNNISRLSVASFNHMPKLRTFR
                                                                                 NNKISKVSPGAFTPLVKLERLYLSKNOLKELPEKM---PKTLQELRAHENEITKVRKVTF
                                                                                                                                                                                                                    PS0001
             LHSNNLLCDCNVAWLSDWLRQRPRLGLYTQCMAPPSLRGHNIAEVQKKEFMCTGPQSHSS
                                                      NGLNOMIVIELGTNPLKSSGIENGAFOGMKKLSYIRIADTNI----
                                                                   ENKISSTERGAFODLOELERLRLNRNNLOVLPELLFLGTTKLFRLDLSENOTOGTPRKAF
                                                                                              CPSQCSCSGTAVDCHGQSLRSVPRNIPRNVERLDLNANNLTKITKADFAGLKNLRVLQLM
                                                                                                                                                                                         PS01186;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Okamoto H.;
                                                                                                                                                                                                                                                                                                                                        IPR000483;
                                                                                                                                                                                                                                                                                                                                                                                     LPRU00152; Asx_hydroxyl.
LPR006207; Cys_knot_C.
LPR000742; EGF_2.
                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                        LRRCT; 4.
                                                                                                                                                                                                                                                                                                      LRR;
                                                                                                                                                      AA;
                                                                                                                                                                                                                                                                                                                                                                                                                         AAG36773.1;
                                                                                                                                                                                                                                                                                                           aminin_G; 1.
                                                                                                                                                                                                                                                                                  EGFBLOOD
                                                                                                                                                                                                                                                                          LEURICHRPT
                                                                                                                                                                     LRR
                                                                                                                                                                                                            ASX HYDROXYL;
CTCK_1; 1.
                                                                                                                                                                                        EGF 2; 8
                                                                                                                                  19.0%;
                                                                                                                                                                                                                                                                                                                        LRR_Nterm.
                                                                                                                                                                                                                                                                                                                                                             EGF_{1ike}.
                                                                                                                                                     166669 MW; 60888COAF0C3D630 CRC64;
                                                                                                                                                                                                                                                                                                                                                     Laminin_G
                                                                                                                                                                  TYPICAL;
                                                                                                                                                                                                                                                                                                                                        LRR Cterm.
                                                                                                                                                                          DOMAIN,
                                                                                                                          54;
                                                                                                                         Score 325; DB
Pred. No. 5.7e-
54; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Craniata; Vertebrata; Euteleostomi; Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Danio
TSIPQGLPPSLTELHLDGNKISRVDAASLKGLNNLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rerio).
                                                                                                                                .7e-14
                                                                                                                                       DB
                                                                                                                          129;
                                                                                                                                       13;
                                                                                                                                                                                                                                                                                                                                                                                                                                 databases
                                                                                                                                       Length 1512;
                                                                                                                          Indels 116;
                                                                                                                         Gaps
218
             258
                                        198
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                           182
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RESULT
075094
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                                                                                             Pfam;
                                                                         Pfam; PF01462; LF PRINTS; PR00019;
                                                                                                     Pfam;
                                                                                                           InterPro; IPRO Pfam; PF00008;
                                                                                                                                                                                                                                                                                                                                                                                             075094;
01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                           075094
                                                                                        Pfam;
                                                                                                                                                                                                                         Genomics
                                                                                                                                                                                                                                                                                Brain
                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1999
01-MAR-2003
                                                                                                                          InterPro;
                                                                                                                               [nterPro;
                                                                                                                                              InterPro;
                                                                                                                                                                  InterPro;
                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                       interPro;
                                                                                                                                                     nterPro;
                                                                                                                                                           nterPro;
                                                                                                                                                                         nterPro;
                                                                                                                                                                                       nterPro;
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                                                                                PF01463;
PF01462;
                                                                                                                                                                                                                                                                                                                                                                                                                                             379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  259
                                                                                                                                                                                                                                                                                Res. Mol.
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Pki.

SMART; SMOOI..

DR SMART; SMOO282; LECT;

DR SMART; SMOO282; LERCT;

DR SMART; SMOO013; LERNT; 4.

DR SMART; SMOO015; LERNT; 4.

PROSITE; PSO0010; ASX HYDROXYL; 2.

PROSITE; PSO1185; CTCK 2; 1.

PROSITE; PSO1225; CTCK 2; 1.

PROSITE; PSO1225; CTCK 2; 1.

PROSITE; PSO1225; CTCK 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-99033071; PubMed-9813312; Itoh A., Miyabayashi T., Ohno M., Sakano S.; "Cloning and expressions of three mammalian slit suggest possible roles for Slit in the of the nervous system.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AB017169; BAA35186.1; -. EMBL; AB011538; BAA32466.1; -. HSSP; P00740; IEDM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLIT-3 protein (MEGF5).
SLIT-3 OR MEGF5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 785-1523 FROM N.A.
TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       like motifs by motif-trap screening."; Genomics 51:27-34(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=99033071;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nakayama M., Nakajima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wakayama M., Nakajima D., Nagase T., Nom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98360089;
                                                                                                   S; PR00019;
S; SM00041; CT; 1.
T; SM00179; EGF CA; 1.
RT; SM00282; LARG; 1.
LRT; SM00082; LARCT; 4.
THOUSE CHART; 4.
THOUSE CHART; 4.
THOUSE CHARTS
                                                                                                                                                                                                                                                                  PF00008; EGF; 9.
PF00054; laminin_G; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HGNC:11087;
                                                                                                                                                                                                                                                                                                                 IPR001611;
IPR000483;
IPR000372;
                                                                                                                                                                                                                                                                                                                                                               IPR001881;
IPR006209;
IPR003006;
IPR001791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSSDFCPPGHNTKKASYSGVSLFSNPVQYWEIQPSTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RIDLSNNQTTELASDSFQGLRSLNSLVLYGNKITELPKGLFDGLFSLQLLLLNANKINCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KLGLSFNSISAVDNGSLANTPHLRELHLDNNKLTRVPGGLAEHKY-IQVVYLHNNNISVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CSVLQCPELCTCSNNVVDCRGKGLTEIPTNLPETITEIRLEQNSIKIIPÄGAFAPYKRLR
                                                                                                                                                                                                                                                                                                                                                                                                                          IPR000152; Asx_hydroxyl.
IPR006207; Cys_knot_C.
IPR000742; EGF_2.
                                                                                                                                                                                                                                                                                                  IPR003591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel.) (TrEMBLrel.) (TrEMBLrel.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                      ; LRRCT;
                                                                                                                                                                                                                                                     LRR; 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brain Res. 62:175-186(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=9693030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLIT3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata; Primates;
                                                                                                                                                                                                                                                                                                                                                                            EGF_Ca.
EGF_like.
Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -QDLQNLNLLSLYDNKLQ--TIAKGTF
                                                                                                                                                                                                                                                                                          LRR_typ.
                                                                                                                                                                                                                                                                                                                   LRR_Cterm.
                                                                                                                                                                                                                                                                                                                                                        Laminin_G.
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11,
23,
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Last sequence update)
Last annotation update)
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Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                              N
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formation a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo
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173 672

732

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RESULT
OBCAGG
AC QG
DT OCCAGG
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Best Local S
Matches 99
                                                                                                                                           Query Match
Best Local S
Matches 95
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PROSITE;
PROSITE;
PROSITE;
EGF-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08CJG9;
                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                              "Alternative splicing for slit-1 in rat brain.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBU databases.
EMBL, AB073214; BAC21465.1;
SEQUENCE 1474 AA; 161314 MW; 82E4CBC2C4B6ED46 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                               SLIT1-Sb splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2003
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2003
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=SD; TISSUE=Brain;
                                                                                                                                                                                                                                                                                    Tanno T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25
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E 1523 AA; 167684 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VCPEKCRCEGTIVDCSNOKLVRIPSHLPBYVTDLRLNDNEVSVLEATGIFKKLPNLRKIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VCPFRCQCHLRVVQCSDLGLDKVPKDLPPDTTLLDLQNNKITEIK-DGDFKNLKNLHALI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RALPRGMPKDVTELYLEGNHLTAV-PRELSALRHLTLIDLSNNSISMLTNYTFSNMSHLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VSGNPRCQKPFFLKEIPIQDVAIQDFTCDGNEESSCQLSPRCPEQCTCMETVVRCSNKGL
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                    IK-DGDFKNLKNLHALILVNNKISKVSPGAFTPLVKLERLYLSKNQLKELPEKMPKTLQE
:: | | | | :| : | | | | :| : | : |
                                                                  LFSNPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELHLDNNKLTRVP----GGLAEHKYIQVVYLHNNNISVVGSSDFCPPGHNTKKASYSGVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----HENETTKVRKVTFNGLNQMIVIELGTNP-----
LEATGLFKKLSHLKKINLSNNKVSEIEDGTFEGATSVSELHLTANQLESVRSGMFRGLDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LGTNPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TLILSYNRLRCIPVHAFNGL---RSLRVLTLHGNDISSV----PEGSFNDLTSLSHLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 (TrEMBLrel. 23, 03) (TrEMBLrel. 23, 03) (TrEMBLrel. 23, 03)
                                                                                                                                       18.9%; Score 324.5; DB llarity 24.6%; Pred. No. 6e-14; Conservative 66; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 859
                                                                                                                                                                                                                                                                                                                                                                                                                                                product
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
Last sequence
Last annotation
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Pred. No. 5.7e-14;
1; Mismatches 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.1.
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52549D41D1D6DBD1 CRC64;
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(on update)
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                                                                                                                                                                          DB 11;
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                                                                                                                                       Indels 103;
                                                                                                                                                                                                              CRC64;
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                                                                                                                                                                          Length 1474;
                                                                                                                                                                                                                                                                                                                                                                        Euteleostomi;
; Murinae; Rattus.
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Best Local S
Matches 95
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Q8CJG8;
Q1-MAR-2003
01-MAR-2003
01-MAR-2003
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NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (I
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLIT1-La
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Alternative splicing for slit-1 Submitted (OCT-2001) to the EMBL, EMBL; AB073215; BAC21666.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tanno T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26
                                                                                                                                         673
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                                                                                                                                                                                                                                                                                    588
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792
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                       003 (TrEMBLrel. 23, Created)
003 (TrEMBLrel. 23, Last sequence update)
003 (TrEMBLrel. 23, Last annotation updat
splicing product (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LRA---HENEITKVRKVTFNGLNQMIVIELGTNPLKSSGIENGAFQGMKKLS-----
                                                                                                                                                                                                                                          LRA---HENEITKVRKVTFNGLNQMIVIELGTNPLKSSGIENGAFQGMKKLS------
                                                                                                                                                                                                                                                                                    LEATGLFKKLSHLKKINLSNNKVSEIEDGTFEGATSVSELHLTANQLESVRSGMFRGLDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNNKISSLSNSSFTNMSQLTTLILSYNALQCIPPLAFQGL---RSLRLLSLHGNDVSTLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SFNSISAVDNGSLANTPHLRELHLDNNKLTRVP----GGLAEHKYIQVVYLHNNNISVVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LRTLMLRNNRISCIHNDSFTGLRNVRLLSLYDNHITTT--SPGÄFDTLQALSTLNLLANP
SNNKISSISNSSFTNMSQLTTLILSYNALQCIPPLAFQGL--
                               SFNSISAVDNGSLANTPHLRELHLDNNKLTRVP----GGLAEHKYIQVVYLHNNNISVVG
                                                                 QCPQECTCLDTVVRCSNKHLQALPKGIPKNVTELYLDGNQFTLV-PGQLSTFKXLQLVDL
                                                                                                                                                                                                                                                                                                                    IK-DGDFKNLKNLHALILVNNKISKVSPGAFTPLVKLERLYLSKNOLKELPEKMPKTLQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FNCNCQLAWLGDWLRKRKIVTGNPRCQNPDLLRQIPLQDVAFPDFRCEEGQEEVGCLPRP
                                                                                                                                       FNCNCQLAWLGDWLRKRKIVTGNPRCHNPDFLRQIPLQDVAFPDFRCEEGQEEVGCLPRP
                                                                                                                                                                                                              1458
1458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                    -YIRIADTNITSIPQGLPPSLTELHLDGNKISRVDAASLKGLNNLAKLGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YIRIADTNITSIPQGLPPSLTELHLDGNKISRVDAASLKGLNNLAKLGL
                                                                                                                                                                                                                                                                                                                                                                                                                                               18.9%;
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10 EMBL/GenBank/DDBJ d
i -.
                                                                                                                                                                                                                                                                                                                                                                                                                              65;
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 323.5;
Pred. No. 6.9e
65; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         304
                                                                                                                                                                                                                                                                                                                                                                                                                        ); DB 11;
5.9e-14;
hes 123;
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Indels

103; 1458

RSLRLLSLHGNDVSTLQ

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732

173 672 173

614

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554 65

CRC64; Length

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RESULT

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                                                                                                                Query Match
Best Local S
Matches 104
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Pfam; PP01463; LRROT; 4.
Pfam; PP01462; LRROT; 4.
Pfam; PF01462; LTRINT; 1.
SMART; SM00041; CT; 1.
SMART; SM00179; EGF CA; 2.
SMART; SM00274; FOLN; 2.
SMART; SM00282; LamG; 1.
                                                                                                                                                                                                                   PROSITE; PS00010; A
PROSITE; PS01185; C
PROSITE; PS01225; C
PROSITE; PS01022; E
PROSITE; PS01186; E
PROSITE; PS50025; I
PROSITE; PS50025; I
PROSITE; PS50066; I
                                                                                                                                                                                                        PROSITE;
EGF-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99033071; PubMed=9813312; Itoh A., Miyabayashi T., Ohno M., Sakano S.; "Cloning and expressions of three mammalian! slit suggest possible roles for slit in the of the nervous system."; Brain Res. Mol. Brain Res. 62:175-186(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         094813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nomo sapieus (numan).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Slit-2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            094813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1999
                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                 ___amG; 1.
__amG; 1.
__amG0013; LRRCT; 4.
__sm000369; LRR TYP; 5.
__sps00010; As___
__; PS00118f
__psc____;
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                                            486
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         64
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p; IPR006207; Cys knot_C.
p; IPR000742; EGF_C.
p; IPR001881; EGF_Ca.
p; IPR0016209; EGF_like.
p; IPR003645; Foli.
                                                                                                                                 Similarity
                                                           VPDDRDFEPSLGP-----VCPFRCQCHLRVVQCSDLGLDKVPKDLPPDTTLLDLQNNKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGIF----ADVTSLSHLAIGANPL 868
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     TEIK-DGDFKNLKNLHALILVNNKISKVSPGAFTPLVKLERLYLSKNQLKELPEKMPKTL
                                       I PGTEDYRSKI SGDCFADLACPEKCRCEGTTVDCSNQKLNKI PEHI PQYTAELRLNNNEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 (TrEMBLrel.
9 (TrEMBLrel.
3 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EGF; 9.
laminin_G; 1.
                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                                           ASX HYDROXYL;
CTCK 1; 1.
CTCK 2; 1.
SEGF 1; 9.
EGF 2; 7.
EGF CA; 2.
                                                                                                                                                                                                                   LAM_G_DOMAIN; 1.
LRR_TYPICAL; 5.
                                                                                                                             18.8%;
                                                                                                                                                                                     169869 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LRR_typ.
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10,
23,
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Last
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                                                                                                            Score 322; DB 4; 1
Pred. No. 9.3e-14;
2; Mismatches 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence update) annotation updat
                                                                                                                                                                                     5D19CC5E7FD461BA CRC64;
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                                                                                                                                              Length 1529;
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                                                                                                            118;
                                                                                                            Gaps
                                         545
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Q8IV47
ID Q8IV4
AC Q8IV4
DT 01-MA
DT 01-MA
DT 01-MA
DT 01-MA
DT 01-MA
CON Homo
OC Eukar
OC Mamma
OX NCEI
RN [1]
RN [1]
RN [1]
RP SEQUI
RC TISSI
RA SETAN
DE SEQUI
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Q9DE37
Q9DE37;
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Query Match
Best Local S
Matches 85
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                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases
EMBL; BC035281; AAH35381.1; -
SEQUENCE 376 AA; 43178 MW; DC19D5E6724AB004 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUB-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TaxID=9606;
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TSIPQGLPPSLTELHLDGNKISRVDAASLKGLNNLAKLGLSFNSISAVDNGSLANT---P
                                                                                                                                                            EIKDGDFKNLKNLHALILVNNKIS--KVSPGAFTPLVKLERLYLSKNQLKELPEKMPKTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNNRISTLSNOSFSNWTQLLTLILSYNKLRCIPPRTFDGL---KSLRLLSLHGNDISVV-
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                                                                       RKVPDGLPSALEQLYMEHNNVYTVPDSYFRGAPKLLYVRLSHNSLT--NNGLASNTFNSS
                                                                                                                                          RELHLDHNQISRVPNNALEGLENLTALYLQHNEIQEVG---SSMRGLRSLILLDLSYNHL
                                                                                                                                                                                                                                                                                 PSPPDPRD-----CPQECDCPPNFPTAMYCDNRNLKYLP-FVPSRMKYVYFQNNQIT
                                                                                                                                                                                                                                                                                                                  PEVPDDRDFEPSLGPVCPFRCQC---HLRVVQCSDLGLDKVPKDLPPDTTLLDLQNNKIT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ESLKTLMLRSNRITCVGNDSFIGLSSVRLLSLYDNQITTVAPGAFDTLHSLSTLNLLANP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLiel. 23, 0) (TrEMBLiel. 23, 1) (TrEMBLiel. 23, 1)
                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -YIRIADTNITSIPOGLPPSLTELHLDGNKISRVDAASLKGLNNLAKLGL
                                                                                                                                                                                                                                                                                                                                                     18.8%; Score 321.5; DB 4
29.9%; Pred. No. 1.7e-14;
tive 55; Mismatches 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                    DB 4;
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   334
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Matches 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000152; Asx hydroxyl.
InterPro; IPR006207; Cys_knot_C.
InterPro; IPR000742; EGF_2.
InterPro; IPR0007481; EGF_Ca.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR0016209; EGF_like.
InterPro; IPR001611; LRR.
InterPro; IPR001611; LRR.
InterPro; IPR000372; LRR_Nterm.
InterPro; IPR000372; LRR_Nterm.
InterPro; IPR003591; LRR_typ.
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01-MAR-2001
01-MAR-2003
Slit3.
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PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
EGF-like
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NCBI_TaxID=7955:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Zebrafish sit3 homolog.";
Submitted (DEC-1999) to the
EMBL; AF210320; AAG36772.1;
HSSP; P00740; 1EDM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZFIN; ZDB-GENE-010306-4; slit3.
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                                                                                                                                                                                                                                                                                 ; ps00010; aSX HYDROXYL; 2
; ps01185; CTCK 1; 1.
; ps01225; CTCK 2; 1.
; ps0022; EGF 1; 9.
; ps01186; EGF 2; 7.
; ps01187; EGF CA; 2.
; ps50125; LAM G DOMAIN; 1
; ps550506; LRR TYPICAL; 5.
                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                               domain.
1515
                                                                                          NNQISVIERGAFEGLKQLERIRLNRNRLQVLPELLFQSTTKLSRLDLSENQIQAVPRKAF
                                                                                                                                     NNKISKVSPGAPTPLVKLERLYLSKNQLKELPEKMPKT----LQELRAHENEITKVRKVTF
                                                                                                                                                                      CPHKCSCSGSHVDCQGQAFKTVPRGIPRNAERLDLDRNNITRITKVDPSGLKNLRVLHLB
                                                                                                                                                                                           CEFRCQCHLRVVQCSDLGLDKVFKDLFPDTTLLDLQNNKITEIKDGDFKNLKNLHALILV
                                                                             RGITTVKNLQLDSNHI--SCIEDGAFRALRDLEILTLNNNNITLIPLSSFNHMPKLRTLR
                                 LHSNNLHCDCHLSWLSDWLRQRRGLAPFTQCMAPAHMRGLNVPDVQKREFVCTGPVETEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rerio (Zebrafish)
Metazoa; Chordata;
                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                               AA;
                                                                                                                                                                                                                             18.6%;
                                                                                                                                                                                                                                                              166871 MW;
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Last
                                                                                                                                                                                                                 Score 318.5; D
Pred. No. 1.6e-
53; Mismatches
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annotation updat
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TSIPQGLPPSLTELHLDGNKISRVDAASLKGL
                                                                                                                                                                                                                             .6e-13
                                                                                                                                                                                                                                      DB 13;
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                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                CRC64;
                                                                                                                                                                                                                                      Length 1515;
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RESULT 30
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Pfam; PP00054; laminin G; 1.
Pfam; PP0146; LRRCT; 4.
Pfam; PP0146; LRRCT; 4.
Pfam; PP0146; LRRWT; 4.
Pfam; PP01462; LRRWT; 4.
SMART; SM0019; EGF CA; 2.
SMART; SM0019; EGF CA; 2.
SMART; SM0029; LARCT; 4.
SMART; SM00028; LRRCT; 4.
SMART; SM00008; LRRCT; 4.
SMART; SM00019; LRRTYP; 8.
SMART; SM00019; LRRTYP; 8.
SMART; SM00019; LRRYTY; 1.
SMART; SM00019; LRRYTY; 1.
SMART; SM00019; LRRYTY; 1.
SMART; SM00019; LRRYTY; 8.
SMART; SM00019; LRRYTY; 1.
PROSITE; PS01186; EGF CA; 2.
PROSITE; PS01186; EGF CA; 2.
PROSITE; PS01187; EGF CA; 2.
PROSITE; PS01187; EGF CA; 2.
PROSITE; PS01187; EGF CA; 2.
PROSITE; PS050025; LRM G DOMAIN
PROSITE; PS05006; LRRTYPICAL;
EGF-Like domain.
SEQUENCE 1521 AA; 168769 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9R1B9;
Q9R1B9;
01-MAY-2000
01-MAY-2000
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99365246; PubMed=10433822;
Yuan W., Zhou L., Chen J.H., Wu J.Y., Rao Y.,
"The mouse SIIT family: secreted ligands for I
patterns that suggest a role in morphogenesis
Dev. Biol. 212:290-306(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Swiss Webster/ICR;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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HSSP; P00743; 1CCF.
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IPR006207; Cys knot_C.
IPR000742; EGF_2.
IPR001881; EGF_Ca.
IPR006209; EGF_like.
IPR003645; FolN.
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Last sequence update)
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Search completed: Job time : 92 secs	Db	γQ	Вb	Ş	Дb	8	Db	Ş	Db	Ş	В	Ş	Ъ	Ş	Query Match Best Local Matches 10
omplete	848	299 1	797	243 1	738 1	183	678	156	618	128	558	83	498	24	
Search completed: February 9, 2004, 11:38:16 Job time : 92 secs	GANPLYCDCNMQWLSDWVKSEYKBPGIARC 878	LESNEVQYMEIQESTERC 316	TLILSYNRLRCIPPRTFDGLKSLRLLSLHGNDISVVPEGAFNDLSALSHLA 847	ELHLDNNKLTRVPGGLAEHKYIQVVYLHNNNISVVGSSDFCPPGHNTKKASYSGVS 298	KVLPKGIPKDVTELYLDGNQFTLV-PKELSNYKHLTLIDLSNNRISTLSNQSFSNMTQLL 796	TSIPQGLPPSLTELHLDGNKISRVDAASLKGLNNLAKLGLSFNSISAVDNGSLANTPHLR 242	TGNPRCQKPYFLKEIPIQDVAIQDFTCDDGNDDNSCSPLSRCPSECTCLDTVVRCSNKGL 737	KSSGIENGAFQGWKKLSYIRIADTNI 182	FIGLGSVRLLSLYDNQITTVAPGAFDSLHSLSTLNLLANPFNCNCHLAWLGEWLRRKRIV 677	HENEITKVRKVTFNGLNQMIVIELGTNP 155	SUNKITDIEEGAFEGASGVNEILLTSNRLENVQHKMFKGLESLKTLMLRSNRISCVGNDS 617	VNNKISKVSPGAFTPLVKLERLYLSKNQLKELPEKMPKTLQELRA 127	CPEKCRCEGTTVDCSNQRLNKIPDHIPQYTAELRLNNNEFTVLEATGIFKKLPQLRKINF 557	CPFRCQCHLRVVQCSDLGLDKVPKDLPPDTTLLDLQNNKITBIK-DGDFKNLKNLHALIL 82	Query Match 18.6%; Score 318; DB 11; Length 1521; Best Local Similarity 25.7%; Pred. No. 1.8e-13; Matches 101; Conservative 59; Mismatches 121; Indels 112; Gaps 11;

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Title:
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

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                1.5 US-10-004-176-6
1.2 US-09-764-875-804
1.2 US-10-319-130-19
1.2 US-10-319-130-19
1.2 US-10-319-318-68
1.5 US-10-177-293-29
1.5 US-09-866-028-2
1.6 US-09-944-457-2
1.0 US-09-944-852-2
1.0 US-09-945-587-2
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              Sequence 6, Appli
Sequence 804, App
Sequence 20, Appl
Sequence 19, Appl
Sequence 68, Appl
Sequence 29, Appli
Sequence 2, Appli
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## ALIGNMENTS

RESULT 1 US-10-004-176-6

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32	Query Match 100.0%; Score 1713; DB 15; Length 329;	9.5
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	LENGTH: 329	~-
	SEQ ID NO 6	 SE ::
	NUMBER OF SEQ ID NOS: 6	
	CURRENT FILING DATE: 2001-11-02	
	FILE REFERENCE: CURRENT APPLICATION NUMBER: US/10/004,176	·· ··
.Q	APPLICANT: Pang, Danny Z. TITLE OF INVENTION: Use of decorin in a cosmetic or dermatological	 H. M
	GENERAL INFORMATION:	። ብ
	Publication No. US20030124152A1	 P 6
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Sequence 20, Application US/10319130
PUDICATION NO. US20030148351A1
GENERAL INFORMATION:
APPLICANT: Henry, Stephen P
APPLICANT: Mayne, Richard
APPLICANT: Hook, Magnus
TITLE OF INVENTION: NUCLEIC ACID AND PROTEIN SEC
FILE REFERENCE: 12740.0234 MPUS02
CURRENT APPLICATION NUMBER: US/10/319,130
CURRENT FILING DATE: 2002-12-13
PRIOR FILING DATE: 2001-12-13
UNMBER OF SEQ ID NOS: 51
NUMBER OF SEQ ID NOS: 51
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Best Local S
Matches 328
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Publication No. US20040018969A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prior application data removed -
NUMBER OF SEQ ID NOS: 1249
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 804
LENGTH: 360
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CURRENT APPLICATION NUMBER: US/09/764,875
CURRENT FILING DATE: 2001-01-17
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PatentIn version 3.2
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                                                                                                                                                                                                                                                                                                                                                NPVQYWEIQPSTFRCVYVRSAIQLGNYK 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           ITSIPQGLPPSLTELHLDGNKISRVDAASLKGLNNLAKLGLSFNSISAVDNGSLANTPHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ITSIPQGLPPSLTELHLDGNKISRVDAASLKGLNNLAKLGLSFNSISAVDNGSLANTPHL 241
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                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 51
SOFTWARE: PatentIn version 3.2
SEQ ID NO 19
LENGTH: 369
TYPE: PRT
ORGANISM: Mus musculus
US-10-319-130-19
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APPLICANT: Mayne, Richard
APPLICANT: Mayne, Richard
APPLICANT: Hook, Magnus
TITLE OF INVENTION: NUCLEIC ACID AND PROTEIN SE
FILE REFERENCE: 12740.0234.NPUS02
CURRENT APPLICATION NUMBER: US/10/319,130
CURRENT FILING DATE: 2002-12-13
PRIOR APPLICATION NUMBER: US 60/341,537
PRIOR PILING DATE: 2001-12-13
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Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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Best Local Similarity
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LENGTH: 354
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TYPE: PRT
ORGANISM: Mus musculus
            160
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                                                                            NNKITEIKDGDFKNLKNLHALIIVNNKISKVSPGAFTPLVKLERLYLSKNQLKBLPEKMP 119
                                      KTLQELRAHENEITKVRKVTFNGLNQMIVIELGTNPLKSSGIENGAFQGMKKLSYIRIAD
                                                                                                                                                  EASGSDTTSGVPDLDSVTPTFSAMCPFGCHCHLRVVQCSDLGLKTVPKBISPDTTLLDLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NPVQYWEIQPSTFRCVYVRSAIQLGNYK 329
           SSLVELRIHDNRIRKVPKGVFSGLRNMNCIEMGGNPLENSGFEPGAFDGL~KLNYLRISE
                                                                                                                                                                                     EASGIGPE - - VPDDRDFEPSLGPVCPFRCQCHLRVVQCSDLGLDKVPKDLPPDTTLLDLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RELHLDNNKLTRVPGGLAEHKYIQVVYLHNNNISVVGSSDFCPPGHNTKKASYSGVSLFS
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                                                                                                                                                                                                                     57.5%; Score 984.5;
57.6%; Pred. No. 7.46
ative 51; Mismatches
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79.9%; Pred. No. 1.2e-119;
tive 28; Mismatches 33;
                                                                                                                                                                                                                                         .4e-84;
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Gaps

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RESULT 6
US-10-177-293-29
; Sequence 29, Application US/10177293
; Publication No. US20030124128A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
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APPLICANT: Jensen, Roderick V.

APPLICANT: Gullans, Steven R.

APPLICANT: Bueno, Raphael

TITLE OF INVENTION: Diagnostic and Prognostic Tele

FILE REFERENCE: B00801/70265 (JRV/JAV)

CURRENT APPLICATION NUMBER: US/10/236,031B

CURRENT FILING DATE: 2002-09-05

PRIOR APPLICATION NUMBER: US 60/317,389

PRIOR FILING DATE: 2001-09-05
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US-10-236-031B-68
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LENGTH: 368
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Publication No.
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Best Local Similarity
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PRIOR FILING DATE: 2002-08-30
NUMBER OF SEQ ID NOS: 102
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TO. US20030219760A1
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57.4%;
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Pred. No. 2.4e-83;
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APPLICANT: SALIA, AVESGUI

APPLICANT: MAILS, GORGON B.

FITTLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT

FILE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER

FILE REFERENCE: MRI-038

CURRENT APPLICATION NUMBER: US/10/177,293

CURRENT FILING DATE: 2002-06-21

PRIOR APPLICATION NUMBER: US 60/299,887

PRIOR PILING DATE: 2001-06-21

PRIOR APPLICATION NUMBER: US 60/301,572

PRIOR APPLICATION NUMBER: US 60/306,501

PRIOR APPLICATION NUMBER: US 60/306,501

PRIOR PILING DATE: 2001-07-18

PRIOR PILING DATE: 2001-09-25

PRIOR APPLICATION NUMBER: US 60/325,002

PRIOR PILING DATE: 2001-09-25

PRIOR PILING DATE: 2001-09-25

PRIOR APPLICATION NUMBER: US 60/362,585

PRIOR PILING DATE: 2001-09-25

PRIOR APPLICATION NUMBER: US 60/362,585
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-293-29
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SOFTWARE: PastSEQ for Windows
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339 NNPVPYWEVQPATERCVTDRLAIQFGNYK 367
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                                                                                                                                                   219 KLTGIPKOLPETLNELHLDHNKIQAIBLEDLLRYSKLYRLGLGHNQIRMIENGSLSFLPT
                                                                                                                                                                                                                                                                                                       100 NDISELRKODPKGLQHLYALVLVNNKISKIHEKAFSPLRKLQKLYISKNHLVEIPPNLPS
                                                                                                                                                                                         181 NITSIPQGLPPSLTELHLDGNKISRVDAASLKGLNNLAKLGLSFNSISAVDNGSLANTPH
                                                                                                                                                                                                                               160 SLVELRIHDNRIRKVPKGVFSGLRNMNCIEMGGNPLENSGFEPGAFDGL-KLNYLRISEA
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                       SNPVQYWEIQPSTFRCVYVRSAIQLGNYK 329
                                                                                             LRELHLDNNKLTRVPGGLAEHKYIQVVYLHNNNISVVGSSDFCPPGHNTKKASYSGVSLF
                                                                         LRELHLDNNKLARVPSGLPDLKLLQVVYLHSNNITKVGVNDFCPMGFGVKRAYYNGISLF
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Monahan, John
Meyers, Rachel E.
Bast Jr., Robert C.
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Wang, Youzhen
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Mertens, Maureen
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Kamatkar, Shubhangi
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Pred. No. 2.4e-83;
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RESULT 7 US-09-866-028-2

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CURRENT FILING DATE: 2001-05-25

Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 120

SEQ ID NO 2

LENGTH: 379

TYPE: PAT TYPE: PAT TYPE: PAT TYPE: PAT TYPE: PAT ORGANISM: Homo Sapien

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US-09-944-449-2
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Patent No. US20020102647A1
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Best Local
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                                                               Baker, Kevin
Botstein, David
                                                                                                                                                                                                                                                                                                                                                                  PSTFRCVYVRSAIQLGNY 328
                                                                                                                                                                                                                                                      LKKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQ 359
                                                                                                                                                                                                                                                                     LTRVPGGLAEHKYIQVVYLHNNNISVVGSSDFCPPGHNTKKASYSGVSLFSNPVQYWEIQ 310
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Tumas, Daniel
Wood, William
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        Ferrara, Napoleone
Filvaroff, Ellen
Gerritsen, Mary
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Goddard, Audrey
                                                      Eaton, Dan
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Grimaldi, Christopher
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APPLICATION NUMBER: 60/075,945
FILING DATE: February 25, 1998
APPLICATION NUMBER: 60/112,850
APPLICATION NUMBER: 60/112,950
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FILING DATE: December 22, 1998
APPLICATION NUMBER: 60/146,222
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                                      APPLICATION
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                                                                                               FILING DATE: June 22, 1999
APPLICATION NUMBER: PCT/US99/21090
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APPLICATION 1
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Roy, Margaret
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Grimaldi, Christopher
X: September 15, 1999

M NUMBER: PCT/US99/28409

TE: NO. US20020102647A1ember 3/

M NUMBER: PCT/US99/28313

TE: NO. US20020102647A1ember 3/

NN NUMBER: PCT/US99/28301
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MIMBER: PCT/US99/12252
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LENGTH: 379
TYPE: PRT
ORGANISM: Homo Sapien
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OR APPLICATION NUMBER: PCT/US00/08439
OR FILING DATE: March 30, 2000
OR FILING DATE: May 22, 2000
OR APPLICATION NUMBER: PCT/US00/14042
OR FILING DATE: May 22, 2000
OR APPLICATION NUMBER: PCT/US00/20710
OR FILING DATE: July 28, 2000
OR APPLICATION NUMBER: PCT/US00/32678
OR APPLICATION NUMBER: PCT/US00/32678
OR APPLICATION NUMBER: PCT/US01/06520
OR APPLICATION NUMBER: PCT/US01/06520
OR FILING DATE: February 28, 2001
BER OF SEQ ID NOS: 120
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APPLICATION NUMBER: PCT/US00/03565
FILING DATE: Pebruary 11, 2000
APPLICATION NUMBER: PCT/US00/04414
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APPLICATION N
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Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
Godowski, Paul
Grimaldi, Christopher
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PATFRCVLSRMSVQLGNF 377
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                           Gurney, Austin
Hillan, Kenneth
Kljavin, Ivar
Napier, Mary
Roy,Margaret
Tumas,Daniel
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NUMBER: PCT/US00/05841
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Pred. No. 5.4e-80;
0; Mismatches 82;
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PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR PILING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
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PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
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DR FILLING DATE: December 12, 1997
DR APPLICATION NUMBER: 60/069,696
DR FILLING DATE: December 16, 1997
DR APPLICATION NUMBER: 60/069,694
DR FILLING DATE: December 16, 1997
DR APPLICATION NUMBER: 60/069,702
DR FILLING DATE: December 16, 1997
DR APPLICATION NUMBER: 60/069,870
DR APPLICATION NUMBER: 60/069,870
DR APPLICATION NUMBER: 60/069,870
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R FILING DATE: February 25, 1998

DR APPLICATION NUMBER: 60/112,850

R FILING DATE: December 16, 1998

DR APPLICATION NUMBER: 60/113,296

R FILING DATE: December 22, 1998
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DR FILLING DATE: December 18, 1997
DR APPLICATION NUMBER: 60/070,440
DR FILLING DATE: January 5, 1998
DR APPLICATION NUMBER: 60/074,086
DR FILING DATE: February 9, 1998
                                              RAPPLICATION NUMBER: PCT/US00/03565
PILING DATE: February 11, 2000
APPLICATION NUMBER: PCT/US00/04414
PILING DATE: February 22, 2000
APPLICATION NUMBER: PCT/US00/04414
PILING DATE: February 22, 2000
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APPLICATION NUMBER: PCT/US99/28409
FILING DATE: No. US20020110859Alember
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FILING DATE: December 16, 1998
APPLICATION NUMBER: 09/218,517
FILING DATE: December 22, 1998
APPLICATION NUMBER: 09/254,311
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FILING DATE: December
APPLICATION NUMBER: 60
FILING DATE: July 28,
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FILING DATE: February 22,
APPLICATION NUMBER: PCT/US
FILING DATE: March 2, 2000
APPLICATION NUMBER: PCT/US
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APPLICATION NUMBER: PCT/US99/21090
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; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR FILING DATE: December 1, 2000
; PRIOR FILING DATE: December 1, 2000
; PRIOR FILING DATE: Pcbruary 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 2
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Homo Sapien
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Best Local Similarity 55.0
Matches 175; Conservative
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APPLICANT: ROY, Margaret
APPLICANT: Tomas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,862
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
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Tumas, Daniel
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Kljavin, Ivar
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FILING DATE: February 9, 1998
APPLICATION NUMBER: 9, 1998
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FILING DATE: No. US20020115145A1ember
APPLICATION NUMBER: PCT/US99/28301
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APPLICATION NUMBER: 60/112,850
FILING DATE: December 16, 1998
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APPLICATION NUMBER: 60/075,94
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FILING DATE: December 17, 1997
APPLICATION NUMBER: 60/068,017
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APPLICATION NUMBER: PCT/US00/32678
                                                                        FILING DATE: May 22, 2000 APPLICATION NUMBER: PCT/US00/20710
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FILING DATE: March 30, 2000
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APPLICATION NUMBER: PCT/US99/30095
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FILING DATE: No. US20020115145A1ember
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FILING DATE: December 11, 1997
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TS: December 16, 1997
N NUMBER: 60/069,702
N DECEMBER 1997
N NUMBER: 60/069,870
N NUMBER: 60/069,870
TS: December 17, 1997
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NUMBER: PCT/US99/12252
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NUMBER: 09/216,
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NUMBER: PCT/US98/25108
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; ORGANISM: Homo Sapien
US-09-944-862-2
CURRENT APPLICATION NUMBER: US/09/945,587
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
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Best Local Similarity
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LENGTH: 379
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                                                                                                                                                                                                              APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548P1C1
                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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Grimaldi, Christopher
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Kljavin, Ivar
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Filvaroff, Ellen
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Q ID NOS: 120
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Pred. No. 5.4e-80;
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                     ; ORGANISM: Homo Sapien 
US-09-945-587-2
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NUMBER OF SEQ 1
SEQ ID NO 2
LENGTH: 379
TYPE: PRT
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                                                                                     FILING DATE: December 1, 2000
APPLICATION NUMBER: PCT/US01/06520
FILING DATE: February 28, 2001
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FILING DATE: Pebruary 22, 2000
APPLICATION NUMBER: PCT/US00/05841
FILING DATE: March 2, 2000
APPLICATION NUMBER: PCT/US00/08439
FILING DATE: March 30, 2000
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APPLICATION NUMBER: PCT/US99/28409
FILING DATE: No. US20020127643Alember 30,
APPLICATION NUMBER: PCT/US99/28313
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FILING DATE: March 3, 1999
APPLICATION NUMBER: PCT/U899/12252
FILING DATE: June 22, 1999
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APPLICATION NUMBER: 09/216,
FILING DATE: December 16, 1
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FILING DATE: July 28, 1999
APPLICATION NUMBER: PCT/US98/19330
FILING DATE: September 16, 1998
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FILING DATE: February 9, 1998
APPLICATION NUMBER: 60/074,092
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                                                                                                                                                                           FILING DATE: May 22, 2000
APPLICATION NUMBER: PCT/US00/20710
FILING DATE: July 28, 2000
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APPLICATION N
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APPLICATION NUMBER: 60/113,296
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APPLICATION NUMBER: 60/
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APPLICATION NUMBER: PCT/US00/03565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US99/30095
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APPLICATION NUMBER: 60/
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                                                                                                                                                        APPLICATION NUMBER: PCT/US00/32678
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                                                                  NOS: 120
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NUMBER: PCT/US99/28301
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Query Match Best Local Similarity Matches 175; Conserv

Conservative

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APPLICANT: Najver, Xodi
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
FILLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FITTLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILLE REFERENCE: P2544891C1
FILLE REFERENCE: P2544891C1
CURRENT FILING DATE: 2001-09-26
FRIOR APPLICATION NUMBER: 60/069, 028
FRIOR APPLICATION NUMBER: 60/067,411
FRIOR APPLICATION NUMBER: 60/067,411
FRIOR FILLING DATE: December 3, 1997
FRIOR APPLICATION NUMBER: 60/069,334
FRIOR FILLING DATE: December 11, 1997
FRIOR APPLICATION NUMBER: 60/069,278
FRIOR APPLICATION NUMBER: 60/069,278
FRIOR APPLICATION NUMBER: 60/069,425
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FRIOR A
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tive 60; Mismatches 82
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; TYPE: PRT
; ORGANISM: Homo 9
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IOR APPLICATION NUMBER: PCT/US98/25108
IOR APPLICATION NUMBER: 09/216,021
IOR FILING DATE: December 1, 1998
IOR APPLICATION NUMBER: 09/218,021
IOR FILING DATE: December 16, 1998
IOR APPLICATION NUMBER: 09/214,311
IOR PILING DATE: December 22, 1998
IOR APPLICATION NUMBER: 09/254,311
IOR FILING DATE: March 3, 1999
IOR APPLICATION NUMBER: PCT/US99/1252
IOR FILING DATE: June 22, 1999
IOR APPLICATION NUMBER: PCT/US99/28409
IOR APPLICATION NUMBER: PCT/US99/28409
IOR APPLICATION NUMBER: PCT/US99/28301
IOR FILING DATE: No. US20020132768Alember 30, 19
IOR APPLICATION NUMBER: PCT/US99/28301
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(OR FILING DATE: December 16, 1999
(OR APPLICATION NUMBER: PCT/US90/03565
(OR FILING DATE: February 11, 2000
(OR APPLICATION NUMBER: PCT/US90/04414
(OR FILING DATE: February 22, 2000
(OR APPLICATION NUMBER: PCT/US90/05941
(OR FILING DATE: March 2, 2000
(OR APPLICATION NUMBER: PCT/US90/08439
(OR FILING DATE: March 30, 2000
(OR APPLICATION NUMBER: PCT/US90/14042
(OR FILING DATE: May 22, 2000
(OR APPLICATION NUMBER: PCT/US90/20710
(OR APPLICATION NUMBER: PCT/US90/20710
(OR FILING DATE: May 28, 2000
(OR APPLICATION NUMBER: PCT/US90/20710
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"E: January 5, 1998
"N NUMBER: 60/074,086
3: February 9, 1998
NUMBER: 60/074,092
Pebruary 9, 1998
NUMBER: 60/075,945
February 25, 1998
NUMBER: 60/112
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Sequence 2 Patent No.

GENERAL INFORMATION:
APPLICANT: Baker, Ke
APPLICANT: Botstein
APPLICANT: Eaton, Da
APPLICANT: Ferrara,
APPLICANT: Filvarof
APPLICANT: Goddard,
APPLICANT: Goddwski
APPLICANT: Godowski
APPLICANT: Grimaldi
APPLICANT: Gurney, A
APPLICANT: Kljavin,
APPLICANT: Kljavin,

Eaton; Dan Botstein, David

Kevin

Gerritsen, Mary Goddard, Audrey Godowski, Paul

Gurney, Austin Hillan, Kenneth Kljavin, Ivar

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                                                      TITLE OF INVENTION: ACIDS ENCODING THE SAME FILL REFERENCE: P2548P1C1

CURRENT APPLICATION NUMBER: US/09/944,396

CURRENT FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: 60/067,411

PRIOR FILING DATE: December 3, 1997

PRIOR PILING DATE: December 11, 1997

PRIOR APPLICATION NUMBER: 60/069,334

PRIOR FILING DATE: December 11, 1997

PRIOR PILING DATE: December 11, 1997

PRIOR PPLICATION NUMBER: 60/069,278

PRIOR PILING DATE: December 11, 1997

PRIOR APPLICATION NUMBER: 60/069,278

PRIOR FILING DATE: December 11, 1997

PRIOR PILING DATE: December 12, 1997

PRIOR APPLICATION NUMBER: 60/069,425

PRIOR PILING DATE: December 12, 1997

PRIOR APPLICATION NUMBER: 60/069,696

PRIOR PILING DATE: December 16, 1997

PRIOR APPLICATION NUMBER: 60/069,696

PRIOR PILING DATE: December 16, 1997

PRIOR APPLICATION NUMBER: 60/069,702

PRIOR PRILING DATE: December 16, 1997

PRIOR APPLICATION NUMBER: 60/069,870

PRIOR PILING DATE: December 17, 1997

PRIOR PILING DATE: December 18, 1997

PRIOR PILING DATE: December 19, 1997
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APPLICANT: Botste:
APPLICANT: Eaton,I
APPLICANT: Ferrar:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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Gurney, Austin
Hillan, Kenneth
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Tumas, Daniel
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Napier, Mary
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; SEQ ID NO 2
**RNGTH: 379
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Best Local Sim
Matches 175;
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PRIOR FILING DATE: February 70
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ICOR FILING DATE: December 16, 1998
IOR APPLICATION NUMBER: 09/218,517
IOR APPLICATION NUMBER: 09/218,517
IOR FILING DATE: December 22, 1998
IOR APPLICATION NUMBER: 09/254,311
IOR FILING DATE: March 3, 1999
IOR APPLICATION NUMBER: 09/254,311
OR FILING DATE: June 22, 1999
OR APPLICATION NUMBER: PCT/US99/12252
OR FILING DATE: June 22, 1999
OR APPLICATION NUMBER: PCT/US99/12252
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IOR FILING DATE: September 15, 1999
IOR APPLICATION NUMBER: PCT/US99/28409
IOR APPLICATION NUMBER: PCT/US99/28419
IOR APPLICATION NUMBER: PCT/US99/28313
IOR APPLICATION NUMBER: PCT/US99/28301
IOR FILING DATE: No. US20020132981A1ember 30, 1999
IOR APPLICATION NUMBER: PCT/US99/28301
IOR APPLICATION NUMBER: PCT/US99/28301
IOR APPLICATION NUMBER: PCT/US99/30095
IOR APPLICATION NUMBER: PCT/US99/30095
IOR APPLICATION NUMBER: PCT/US99/30565
IOR FILING DATE: Pebruary 11, 2000
IOR FILING DATE: Pebruary 11, 2000
IOR FILING DATE: Pebruary 11, 2000
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APPLICATION NUMBER: PCT/US98/
FILING DATE: September 16, 19
APPLICATION NUMBER: PCT/US98/
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APPLICATION NUMBER: PCT/US00/14042
FILING DATE: May 22, 2000
APPLICATION NUMBER: PCT/US00/20710
FILING DATE: July 28, 2000
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FILING DATE: December 22, 1998
APPLICATION NUMBER: 60/146,222
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FILING DATE: February
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FILING DATE: March 2,
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                   FKNLKNILHALILVNNKISKVSPGAFTPLVKLERLYLSKNQLKELPEKMPKTLQELRAHEN 130
                                                                                                                                                                                        PRSHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKEND
                                                                                                                                                                                                                    PDDRDFEPSLGPVCPFRCQCHLRVVQCSDLGLDKVPKDLPPDTTLLDLQNNKITEIKDGD
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NUMBER: PCT/US98/19330
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NUMBER: PCT/US00/05841
                                                                                                                                                                                                                                                                       55.1%; Score 943.5; DB 1
55.0%; Pred. No. 5.4e-80;
tive 60; Mismatches 82
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRAN TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P2548F1C1
CURRENT APPLICATION NUMBER: US/09/944,097
CURRENT APPLICATION NUMBER: 60/069,334
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILLING DATE: 2001-05-25
PRIOR FILLING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,355
PRIOR FILLING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILLING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,475
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILLING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR FILLING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,694
PRIOR FILLING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,897
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PRIOR APPLICATION NUMBER: 60/069,897
PRIOR APPLICATION NUMBER: 60/069,870
PRIOR FILLING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069,870
PRIOR FILLING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069,870
PRIOR FILLING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/069,870
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US-09-944-097-2
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                                                                       FILING DATE: February 9, 19
APPLICATION NUMBER: 60/075,
FILING DATE: February 25, 1
APPLICATION NUMBER: 60/112,
                                                                                                                                                                                                           FILING DATE: December 18, 1997
APPLICATION NUMBER: 60/070,440
FILING DATE: January 5, 1998
APPLICATION NUMBER: 60/074,086
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Tumas, Daniel
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Grimaldi, Christopher
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Hillan, Kenneth
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; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-097-2
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LENGTH: 379
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Best Local Sim
Matches 175;
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(OR APPLICATION NUMBER: PCT/US99/12252

(OR FILING DATE: June 22, 1999

(OR APPLICATION NUMBER: PCT/US99/21090

(OR APPLICATION NUMBER: PCT/US99/28409

(OR APPLICATION NUMBER: PCT/US99/28413

(OR APPLICATION NUMBER: PCT/US99/28113

(OR APPLICATION NUMBER: PCT/US99/28113

(OR APPLICATION NUMBER: PCT/US99/28301

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RAPLICATION NUMBER: PCT/US00/05841

RAPLICATION NUMBER: PCT/US00/08439

RAPLICATION NUMBER: PCT/US00/08439

RAPLICATION NUMBER: PCT/US00/14042

RAPLICATION NUMBER: PCT/US00/14042

RAPLICATION NUMBER: PCT/US00/14042
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APPLICATION NUMBER: 09/218,517
FILING DATE: December 22, 1998
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APPLICATION NUMBER: PCT/US00/04414
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APPLICATION NUMBER: PCT/US99/30095
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APPLICATION NUMBER: PCT/US98/25108
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PSTFRCVYVRSAIQLGNY 328
                                                                                                                                                       PSLTELHLDGNKISRYDAASLKGLNNLAKLGLSFNSISAVDNGSLANTPHLRELHLDNNK 250
                                                                  LKKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQ
                                                                                       LTRVPGGLAEHKYIQVVYLHNNNISVVGSSDFCPPGHNTKKASYSGVSLFSNPVQYWEIQ 310
                                                                                                                                                                                                                                                                                                                                         FKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHEN
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RESULT 15 US-09-944-432-2

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Sequence 2, Application US/09944432 Patent No. US20020142419A1
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P254891C1
CURRENT APPLICATION NUMBER: US/09/944,432
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR PRIOR PILING DATE: December 3, 1997
PRIOR PILING DATE: December 3, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
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                                                   FILING DATE: 00/146, 442
FILING DATE: July 28, 1999
FILING TATE: July 28, 1998/19330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/069,278 FILING DATE: December 11, 1997
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FILING DATE: December 11, 199
                                                 APPLICATION NUMBER: FILING DATE: Septem
                                                                                                               APPLICATION NUMBER: 60
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FILING DATE: February 9, 1998
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              APPLICATION NUMBER: PCT/US98/25108 FILING DATE: December 1, 1998
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Grimaldi, Christopher
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Tumas, Daniel
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Hillan, Kenneth
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US-09-944-432-2
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SEQ ID NO 2
LENGTH: 379
TYPE: PRT
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OR APPLICATION NUMBER: PCT/USO0/03565
OR FILING DATE: February 11, 2000
OR APPLICATION NUMBER: PCT/USO0/04414
OR FILING DATE: February 22, 2000
OR APPLICATION NUMBER: PCT/USO0/05841
OR APPLICATION NUMBER: PCT/USO0/05841
OR FILING DATE: MATCh 2, 2000
OR APPLICATION NUMBER: PCT/USO0/08439
OR FILING DATE: MATCh 30, 2000
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FILING DATE: February 28
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FILING DATE: May 22, 2000
APPLICATION NUMBER: PCT/US00/20710
FILING DATE: July 28, 2000
APPLICATION NUMBER: PCT/US00/32678
FILING DATE: December 1, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US99/28409
FILING DATE: No. US20020144419A.ember 30,
APPLICATION NUMBER: PCT/US99/28313
FILING DATE: No. US20020142419A1ember 30,
APPLICATION NUMBER: PCT/US99/28301
FILING DATE: December1, 1999
APPLICATION NUMBER: PCT/US99/30095
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APPLICATION NUMBER: 09/254,311
FILING DATE: March 3, 1999
APPLICATION NUMBER: PCT/US99/12252
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PATFRCVLSRMSVQLGNF 377
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)S: 120
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Pred. No. 5.4
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RESULT 16
US-09-943-762-2
US-09-943-762-2
; Sequence 2, Application US/09943762
; Patent No. US20020142958A1
; GENERAL INFORMATION:

359

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APPLICANT: WOOD, WILLIAM
TITLE OF INVENTION: SECRETED AND TRANSMEMBRA
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/943,762
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,225
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,225
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,225
PRIOR FILING DATE: December 11, 1997
PRIOR PRIOR FILING DATE: DECEMBER: 60/069,425
PRIOR FILING DATE: DECEMBER: 60/069,425
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          R FILING DATE:
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R FILING DATE:
                                                               APPLICATION NUMBER: 09/218,517
APPLICATION NUMBER: 09/218,517
FILING DATE: December 22, 1998
APPLICATION NUMBER: 09/254,311
FILING DATE: March 3, 199
APPLICATION NUMBER: PCT/US99/12252
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APPLICATION NUMBER: 60/074,092
TITING DATE: February 9, 1998
TITING DATE: February 9, 1998
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FILING DATE: December 18, 1997
APPLICATION NUMBER: 18, 1997
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FILING DATE: December 16, 1997
APPLICATION NUMBER: 60/069,702
FILING DATE: December 16, 1997
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APPLICATION NUMBER: 60/075,945
APPLICATION February 25, 1998
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FILING DATE: December 12, 1997
APPLICATION NUMBER: 60/069,696
FILLING DATE: December 16, 1997
                                                                                                                                                                      APPLICATION NUMBER: 09/216,021 FILING DATE: December 16, 1998
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FILING DATE: July 28, 1999
APPLICATION NUMBER: PCT/US98/19330
                                                                                                                                                                                                                                                                                                                                          FILING DATE: December 16, 1998
APPLICATION NUMBER: 60/113,296
FILING DATE: December 22, 1998
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Roy, Margaret
Tumas, Daniel
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Grimaldi, Christopher
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Goddard, Audrey
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Filvaroff, Ellen
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Botstein,David
      NUMBER: PCT/U
September 15
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                                                                                                                            RESULT 17
US-09-944-654-2
; Sequence 2, Application US/09944654
; Patent No. US20020142959A1
; GENERAL INFORMATION:
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                                                                                GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleo
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Best Local
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OR APPLICATION NUMBER: PCT/US00/05841
OR PILING DATE: March 2, 2000
OR APPLICATION NUMBER: PCT/US00/08439
OR FILING DATE: March 30, 2000
OR APPLICATION NUMBER: PCT/US00/14042
OR APPLICATION NUMBER: PCT/US00/20710
OR APPLICATION NUMBER: PCT/US00/20710
OR APPLICATION NUMBER: PCT/US00/32678
OR APPLICATION NUMBER: PCT/US00/32678
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EAPPLICATION NUMBER: PCT/US00/03565
FILING DATE: February 11, 2000
A APPLICATION NUMBER: PCT/US00/04414
APPLICATION PAPER: PCT/US00/04414
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FILING DATE: No. US20020142958Alember 30, 1999
APPLICATION NUMBER: PCT/US99/28313
FILING DATE: No. US20020142958Alember 30, 1999
APPLICATION NUMBER: PCT/US99/28301
FILING DATE: December1, 1999
APPLICATION NUMBER: PCT/US99/30095
FILING DATE: December 1, 1999
APPLICATION NUMBER: PCT/US99/30095
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Ferrara, Napoleone
Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
Godowski, Paul
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55.0%; Pred. No. 5.4e
tive 60; Mismatches
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Indels Length

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CURRENT APPLICATION NUMBER: US/09/94.
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
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TITLE OF INVENTION: SECRETED
TITLE OF INVENTION: ACIDS EN
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             IOR FILING DATE: December 22, 1998
IOR APPLICATION NUMBER: 09/254,311
IOR APPLICATION NUMBER: 09/254,311
IOR FILING DATE: MARCH 3, 1999
IOR APPLICATION NUMBER: PCT/US99/1252
IOR FILING DATE: June 22, 1999
IOR APPLICATION NUMBER: PCT/US99/21090
IOR FILING DATE: September 15, 1999
IOR APPLICATION NUMBER: PCT/US99/28409
IOR APPLICATION NUMBER: PCT/US99/28301
IOR FILING DATE: No. US20020142959Alember 30, 1999
IOR APPLICATION NUMBER: PCT/US99/28301
IOR FILING DATE: No. US20020142959Alember 30, 1999
IOR APPLICATION NUMBER: PCT/US99/30095
IOR APPLICATION NUMBER: PCT/US99/30095
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APPLICATION NUMBER: 60/
FILING DATE: December 1
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FILING DATE: December 11, 1997
APPLICATION NUMBER: 60/069335
FILING DATE: December 11, 1997
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FILING DATE: December 1
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FILING DATE: December 1
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FILING DATE: December 16, 1998
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APPLICATION NUMBER: PCT/US98/25108
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APPLICATION NUMBER: PCT/US98/19330
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APPLICATION NUMBER: 60/112,850
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Tumas, Daniel
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Gurney, Austin
Hillan, Kenneth
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; TYPE: PRT
; ORGANISM: Homo S
US-09-944-654-2
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PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR PELING DATE: March 30, 2000
PRIOR PELING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR PILING DATE: July 28, 2000
PRIOR PILING DATE: DCT/US00/32678
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
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Matches 175
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APPLICANT:
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FILING DATE: February 11, 2000
APPLICATION NUMBER: PCT/US00/04414
FILING DATE: February 22, 2000
APPLICATION NUMBER: PCT/US00/05841
                                                                                                                                                                                                                                                                                                INFORMATION:
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                                                                                                                            Gerritsen, Mary
Goddard, Audrey
Godowski, Paul
Grimaldi, Christopher
                                                                                        Gurney, Austin
Hillan, Kenneth
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                                                                                                                                                                                                                                                            Botstein, David
Wood, William
             Roy,Margaret
Tumas,Daniel
                                                   Napier, Mary
                                                                        Kljavin, Ivar
                                                                                                                                                                                                     Ferrara, Napoleone
Filvaroff, Ellen
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Pred. No. 5.4
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379; ۳.

Gaps

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299

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CURRENT FILING DATE: 2001-08-30 PRIOR APPLICATION NUMBER: US/09/866,028 PRIOR FILING DATE: 2001-05-25
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(OR FILING DATE: December 22, 1998
(OR APPLICATION NUMBER: 09/254,311
OR FILING DATE: March 3, 1999
OR APPLICATION NUMBER: PCT/US99/12252
OR FILING DATE: March 3, 1999
OR APPLICATION NUMBER: PCT/US99/12252
OR FILING DATE: June 22, 1999
OR APPLICATION NUMBER: PCT/US99/12252
        OR FILING DATE: February 11, 2000
OR APPLICATION NUMBER: PCT/US00/04414
OR FILING DATE: February 22, 2000
OR APPLICATION NUMBER: PCT/US00/05841
OR FILING DATE: March 2, 2000
OR APPLICATION NUMBER: PCT/US00/08439
OR FILING DATE: March 30, 2000
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PILICATION NUMBER: 60/146,222
PILING DATE: July 28, 1999
APPLICATION NUMBER: 60/146,222
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ENT APPLICATION NUMBER: US/09/943,851A
                                                                                                                                              FILING DATE: December 16, 1999
APPLICATION NUMBER: PCT/US00/03565
                                                                                                                                                                 FILING DATE: December1, 1999
APPLICATION NUMBER: PCT/US99/30095
FILING DATE: December 16, 1999
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FILING DATE: No. US20020150976A1ember 30, APPLICATION NUMBER: PCT/US99/28301
FILING DATE: December1, 1999
FILING DATE: December1, 1999
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APPLICATION NUMBER: PCT/US99/21090
FILING DATE: September 15, 1999
APPLICATION NUMBER: PCT/US99/28409
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APPLICATION NUMBER: 09/
TWY THIS DATE: December 1
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FILING DATE: December 16, 1997
APPLICATION NUMBER: 60/069,694
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FILING DATE: December 12, 1997
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FILING DATE: December 3, 1997
APPLICATION NUMBER: 60/069,334
FILING DATE: December 11, 1997
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APPLICATION NUMBER: 60/113,296
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APPLICATION NUMBER: 60/074,092
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FILING DATE: December 11, 199
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OF INVENTION: ACIDS ENCODING THE SAME
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NUMBER: PCT/US98/19330
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APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Mood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POI
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P254891C1
CURRENT APPLICATION NUMBER: US/09/944,413
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR APPLICATION NUMBER: 60/067,411
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Patent No. US20020156004A1
GENERAL INFORMATION:
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Best Local Similarity
Matches 175; Conserv
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TYPE: PRT
ORGANISM: Homo
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OR FILING DATE: May 22, 2000
OR APPLICATION NUMBER: PCT/US00/20710
OR FILING DATE: July 28, 2000
OR APPLICATION NUMBER: PCT/US00/32678
OR RILING DATE: December 1, 2000
OR APPLICATION NUMBER: PCT/US01/06520
OR APPLICATION NUMBER: PCT/US01/06520
OR FILING DATE: February 28, 2001
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Filvaroff, Ellen
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OR FILING DATE: March 2, 2000
OR APPLICATION NUMBER: PCT/US00/08439
OR FILING DATE: March 30, 2000
OR APPLICATION NUMBER: PCT/US00/14042
OR FILING DATE: May 22, 2000
OR APPLICATION NUMBER: PCT/US00/20710
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APPLICATION NUMBER: PCT/US99/21090
FILING DATE: September 15, 1999
APPLICATION NUMBER: PCT/US99/28409
FILING DATE: No. US20020156004Alember
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APPLICATION NUMBER: 60/11.
APPLICATION NUMBER: PCT/US98/19330
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APPLICATION NUMBER: 60/074,086
FILING DATE: February 9, 1998
APPLICATION NUMBER: 60/074,092
FILING DATE: February 9, 1998
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APPLICATION NUMBER: PCT/US00/04414
TITTED NAME: February 22, 2000
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APPLICATION NUMBER: PCT/US99/30095
FILING DATE: December 16, 1999
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FILING DATE: MATCH 3, 1999
APPLICATION NUMBER: PCT/US99/12252
FILING DATE: June 22, 1999
FILING DATE: December 1, 2000
APPLICATION NUMBER: PCT/US01/06520
FILING DATE: February 28, 2001
                                                                            FILING DATE: July 28, 2000
APPLICATION NUMBER: PCT/US00/32678
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APPLICATION NUMBER: PCT/US00/03565
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FILING DATE: No. US20020156004A1ember
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NUMBER: PCT/US00/05841
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US-09-944-403-2
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US-09-944-413-2
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; SEQ ID NO 2
; LENGTH: 379
; TYPE: PRT
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Best Local Similarity
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APPLICANT: Wood, William
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,403
CURRENT FILING DATE: 2001-09-26
                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
           OR APPLICATION NUMBER: 09/866,028
OR FILING DATE: 2001-05-25
OR APPLICATION NUMBER: 60/067,411
OR APPLICATION NUMBER: 60/069,334
OR APPLICATION NUMBER: 61/069,334
OR FILING DATE: December 11, 1997
OR APPLICATION NUMBER: 60/069335
OR FILING DATE: December 11, 1997
OR APPLICATION NUMBER: 60/069,278
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US20020165143A1
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                                                                                                                                                                                                                                                                                    Roy, Margaret
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Hillan, Kenneth
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Grimaldi, Christopher
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Filvaroff, Ellen
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APPLICATION NUMBER: 60/ FILING DATE: December 1 APPLICATION NUMBER: 60/

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NUMBER: 60/069,

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; LENGTH: 379
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; ORGANISM: Homo Sapien
US-09-944-403-2
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NUMBER OF SEQ
; SEQ ID NO 2
rength: 379
               Query Match
                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
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OR FILING DATE: MARCH 3, 1999

(OR APPLICATION NUMBER: PCT/US99/12252

(OR FILING DATE: June 22, 1999

(OR APPLICATION NUMBER: PCT/US99/21090

(OR APPLICATION NUMBER: PCT/US99/28409

(OR APPLICATION NUMBER: POT/US99/28409

(OR APPLICATION NUMBER: POT/
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OR APPLICATION NUMBER: 60/070, 440
OR FILING DATE: January 5, 1998
OR APPLICATION NUMBER: 60/074,086
OR FILING DATE: Pebruary 9, 1998
OR APPLICATION NUMBER: 60/074,092
OR FILING DATE: Pebruary 9, 1998
OR APPLICATION NUMBER: 60/075,945
OR FILING DATE: Pebruary 25, 1998
OR APPLICATION NUMBER: 60/112,850
OR FILING DATE: December 16, 1998
OR APPLICATION NUMBER: 60/113,296
OR APPLICATION NUMBER: 60/1146,222
OR FILING DATE: December 16, 1998
OR APPLICATION NUMBER: PCT/US98/1933
OR APPLICATION NUMBER: PCT/US98/1933
OR APPLICATION NUMBER: PCT/US98/1933
OR FILING DATE: September 16, 1998
OR APPLICATION NUMBER: 09/216,021
OR APPLICATION NUMBER: 09/218,517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: February 22, 2000
APPLICATION NUMBER: PCT/US00/05841
FILING DATE: March 2, 2000
APPLICATION NUMBER: PCT/US00/08439
FILING DATE: March 30, 2000
FILING DATE: March 30, 2000
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APPLICATION NUMBER: PCT/US00/20710
FILING DATE: July 28, 2000
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APPLICATION NUMBER: PCT/US00/04414
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APPLICATION NUMBER: PCT/US99/30095
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FILING DATE: No. US20020165143A1ember 30,
APPLICATION NUMBER: PCT/US99/28301
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APPLICATION NUMBER: 60/068,017
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APPLICATION NUMBER: 60/069,873
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                                                                                                             CURRENT APPLICATION NUMBER: US/09/944,896
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR PILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069335
PRIOR FILING DATE: December 11, 1997
PRIOR PILING DATE: December 12, 1997
PRIOR PILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR PILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,626
PRIOR PILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,626
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,626
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Patent No. US2003
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548P1C1
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                                                        DR FILING DATE: December 11, 1997
DR APPLICATION NUMBER: 60/069,425
DR FILING DATE: December 12, 1997
DR APPLICATION NUMBER: 60/069,696
DR FILING DATE: December 16, 1997
DR APPLICATION NUMBER: 60/069,694
DR FILING DATE: December 16, 1997
DR APPLICATION NUMBER: 60/069,702
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Tumas, Daniel
Wood, William
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Hillan, Kenneth
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Filvaroff, Ellen
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; NUMBER OF SEQ ID NOS: 12; SEQ ID NO 2; LENGTH: 379; TYPE: PRT; ORGANISM: Homo Sapien US-09-944-896-2
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Matches 175
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PRIOR FILING DATE: December 1, 2000
PRIOR PPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: Pebruary 29
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IOR FILING DATE: December 22, 1998
OR APPLICATION NUMBER: 09/254,311
OR FILING DATE: March 3, 1999
OR APPLICATION NUMBER: PCT/US99/12252
DR FILING DATE: June 22, 1999
DR APPLICATION NUMBER: PCT/US99/12252
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FILING DATE: February 25, 1998
APPLICATION NUMBER: 60/112,850
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FILING DATE: July 28,
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APPLICATION NUMBER: PCT/US00/05841
FILING DATE: March 2, 2000
APPLICATION NUMBER: PCT/US00/08439
FILING DATE: March 30, 2000
APPLICATION NUMBER: PCT/US00/14042
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APPLICATION NUMBER: PCT/US99/30095
FILING DATE: December 16, 1999
APPLICATION NUMBER: PCT/US00/03565
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FILING DATE: September 15, 1999
APPLICATION NUMBER: PCT/US99/28409
FILING DATE: NO. US20020168715A1ember 30, 1999
APPLICATION NUMBER: PCT/US99/28313
FILING DATE: NO. US20020168715A1ember 30, 1999
APPLICATION NUMBER: PCT/US99/28301
FILING DATE: NO. US20020168715A1ember 30, 1999
APPLICATION NUMBER: PCT/US99/28301
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APPLICATION NUMBER: PCT/US98/25108
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                                                                                                                                55.1%; Score 943.5; DB 10; 55.0%; Pred. No. 5.4e-80; tive 60; Mismatches 82;
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Sequence 2, Application US/09944944 Patent No. US20020173463A1
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APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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APPLICATION NUMBER: 60/069,425
December 12, 1997
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NT EILING DATE: 2001-09-26
APPLICATION NUMBER: 09/866,028
FILING DATE: 2001-05-25
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APPLICATION NUMBER: 60/069,278
December 11, 1997
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APPLICATION NUMBER: 60/
FILING DATE: December 1
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                                                                                                               APPLICATION NUMBER: 60/069,870 FILING DATE: December 17, 1997 APPLICATION NUMBER: 60/069,873
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FILING DATE: December 16, 1997
APPLICATION NUMBER: 60/069,702
FILING DATE: December 16, 1997
APPLICATION NUMBER: 60/074
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Godowski, Paul
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Roy, Margaret
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Hillan, Kenneth
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Filvaroff, Ellen
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US-09-944-944-2
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SEQ ID NO 2
LENGTH: 379
TYPE: PRT
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Best Local (
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PRIOR FILING DATE: February 28 2001
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(OR APPLICATION NUMBER: 09/254,311
(OR FILING DATE: March 3, 1992)
(OR APPLICATION NUMBER: PCT/US99/12252
(OR FILING DATE: June 22, 1999
(OR APPLICATION NUMBER: PCT/US99/21090
(OR FILING DATE: September 15, 1999
(OR APPLICATION NUMBER: PCT/US99/28409
(OR FILING DATE: NO. US20020173463Alember 30
(OR APPLICATION NUMBER: PCT/US99/28313
(OR FILING DATE: NO. US20020173463Alember 30
(OR APPLICATION NUMBER: PCT/US99/28301
(OR APPLICATION NUMBER: PCT/US99/30095
(OR APPLICATION NUMBER: PCT/US99/20007
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(OR APPLICATION NUMBER: PCT/US99/
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FILING DATE: March 2, 2000
APPLICATION NUMBER: PCT/US00/08439
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FILING DATE: December 16, 1998
APPLICATION NUMBER: 09/218,517
FILING DATE: December 22, 1998
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APPLICATION NUMBER: PCT/US98/19330
FILING DATE: September 16, 1998
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APPLICATION NUMBER: PCT/US00/14042
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APPLICATION NUMBER: PCT/US00/04414
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APPLICATION NUMBER: PCT/US00/20710
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PTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVRBIHLENNK
                       PSLTELHLDGNKISRVDAASLKGLNNLAKLGLSFNSISAVDNGSLANTPHLRELHLDNNK 250
                                                                                                           FKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNOLSEIPLNLPKSLAELRIHEN
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Pred. No. 5.4e
60; Mismatches
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5.4e-80;
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; ORGANISM: Homo
US-09-944-929-2
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US-09-944-929-2
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PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 2
LENGTH: 379
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APPLICANT: Wood, William
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,929
CURRENT FILLING DATE: 2001-08-31
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Grimaldi, Christopher
Gurney, Austin
Hillan, Kenneth
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PATFRCVLSRMSVQLGNF
PATERCVLSRMSVQLGNF 377
                    PSTFRCVYVRSAIQLGNY 328
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Pred. No. 5.4e-80;
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; ORGANISM: Homo
US-09-944-907-2
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APPLICANT: Baker, K
APPLICANT: Botstel;
APPLICANT: Eaton, D
APPLICANT: Ferrara
APPLICANT: Filvaro
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TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,907
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR PILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 2
LENGTH: 379
TYPE: DET
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Sequence 2, Application US/09944884
Publication No. US20030077698A1
GENERAL INFORMATION:
APPLICANT: Bactar, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
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Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
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Tumas, Daniel
Wood, William
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Kljavin, Ivar
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Grimaldi, Christopher
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Pred. No. 5.4e-80;
0; Mismatches 82;
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US-09-944-852-2
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; ORGANISM: Homo
US-09-944-884-2
                                                                                                                                                                                                                 Sequence 2, Application No. US200: Publication No. US200: GENERAL INFORMATION: Baker, Key APPLICANT: Batestein, APPLICANT: Baton, Dat APPLICANT: Ferrara,
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Best Local :
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CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 120
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Godowski, Paul
Grimaldi, Christopher
Gurney, Austin
Hilan, Kenneth
Kljavin, Ivar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDDRDFEPSLGPVCPPRCQCHLRVVQCSDLGLDKVPKDLPPDTTLLDLQNNKITEIKDGD
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Tumas, Daniel
Wood, William
                                                                                                                                                                                                                                                                                                                                                         Application US/09944852 No. US20030083479A1
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Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
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Goddard, Audrey
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Hillan, Kenneth
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Grimaldi,Christopher
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                                                                                                                                                                                                                                                 Eaton, Dan
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Pred. No. 5.4
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RESULT 27
US-09-943-780-2
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TYPE: PRT
ORGANISM: Homo Sapien
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Publication
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Best Local Similarity
Matches 175; Conserv
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      APPLICANT: Tumas, Däniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
FITTE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548PIC1
CURRENT APPLICATION NUMBER: US/09/943,780
CURRENT FILING DATE: 2001-09-26
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548PIC1
CURRENT APPLICATION NUMBER: US/09/944,852
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
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                                                                                                                                                                                                                               Ferrara, Napoleone
Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                        Application US/09943780
No. US20030096742A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BITKVRKVTFNGLNOMIVIELGTNPLKSSGIENGAFQGMKKLSYIRIADTNITSIPQGLP 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LKKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LTRVPGGLAEHKYIQVVYLHNNNISVVGSSDFCPPGHNTKKASYSGVSLFSNPVQYWEIQ 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FKGLTSLYGLILNNKLTKIHPKAFLTTKKLRLYLSHNQLSEIPLNLPKSLABLRIHEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FKNLKNLHALILVNNKISKVSPGAFTPLVKLERLYLSKNQLKELPEKMPKTLQELRAHEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PDDRDFEPSLGPVCPFRCQCHLRVVQCSDLGLDKVPKDLPPDTTLLDLQNNKITEIKDGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSTFRCVYVRSAIQLGNY 328
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Roy, Margaret
Tumas, Daniel
Wood, William
                                                                                                                                                                Gurney, Austin
Hillan, Kenneth
                                                                                                                   Napier, Mary
Roy, Margaret
                                                                                                                                                   Kljavin, Ivar
                                                                                                                                                                                              Godowski, Paul
Grimaldi, Christopher
                                                                                                                                                                                                                                                                                                           Botstein, David
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Pred. No. 5.4e-80;
0; Mismatches 82
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OR APPLICATION NUMBER: 09/216,021
OR APPLICATION NUMBER: 09/210,517
OR FILING DATE: December 22, 1998
OR APPLICATION NUMBER: 09/254,311
OR APPLICATION NUMBER: 09/254,311
OR FILING DATE: March 3, 1999
OR APPLICATION NUMBER: 9CT/US99/1252
OR FILING DATE: June 22, 1999
OR APPLICATION NUMBER: PCT/US99/12090
              FILING DATE: March 30, 2000
APPLICATION NUMBER: PCT/US00/14042
FILING DATE: May 22, 2000
APPLICATION NUMBER: PCT/US00/20710
FILING DATE: July 28, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: February 25, 1998
APPLICATION NUMBER: 60/112,850
FILING DATE: December 16, 1998
APPLICATION NUMBER: 60/113,296
FILING DATE: December 22, 1998
                                                                                         APPLICATION NUMBER: PCT/US00/05841 FILING DATE: March 2, 2000 APPLICATION NUMBER: PCT/US00/08439
                                                                                                                                                                                     FILING DATE: December 16, 1999
APPLICATION NUMBER: PCT/US00/03565
                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US99/28313
FILING DATE: No. US20030096742Alember
APPLICATION NUMBER: PCT/US99/28301
FILING DATE: December1, 1999
APPLICATION NUMBER: PCT/US99/30095
FILING DATE: December 16, 1999
                                                                                                                                          FILING DATE:
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                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US99/28409
FILING DATE: No. US20030096742A1ember
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: December 22, 1998 APPLICATION NUMBER: 60/146,222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: January 5, 1998
APPLICATION NUMBER: 60/074,08
FILING DATE: February 9, 1998
APPLICATION NUMBER: 60/074,09
FILING DATE: February 9, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 18, 199
APPLICATION NUMBER: 60/070,44
APPLICATION NUMBER: 5, 1998
                                                                                                                                                                        FILING DATE: February 11,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: September 16, 1998
APPLICATION NUMBER: PCT/US98/25108
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FILING DATE:
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LING DATE: September 15,
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September 16
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PCT/US00/32678
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; LENGTH: 379
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-943-780-2
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; ORGANISM: Homo Sapien
US-10-137-870-328
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US-10-137-870-328
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Best Local Similarity
Matches 175; Conserv
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PRIOR APPLICATION NUMBER: PCT/USO1/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 2
                           CURRENT APPLICATION NUMBER: US/10/137,870
CURRENT FILING DATE: 2002-05-03
Prior Application removed - See Palm or Fi
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 328
LENCTH: 379
TYPE: PRT
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APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maur
APPLICANT: DeForge, Laura
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                                                                                                                                    TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C155
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Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
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                                                                                                                                                                                            Tumas, Daniel
Watanabe, Colin K
Wood, William
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                                                                                                                                                                                 Zhang, Zemin
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                                                                                                                                                                                                                                             Stewart, Timothy A.
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Pred. No. 5.4e-80;
                                                                                        Palm or File
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                                                                                                             ; TYPE: PRT; ORGANISM: Homo Sapien US-10-140-018-328
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                                                                                                                                                    Prior Application removed -
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 328
LENGTH: 379
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                                                         Matches
                                                                   Query Match
Best Local
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Best Local Similarity
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APPLICANT:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3330R1C158
                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/140,018
CURRENT FILING DATE: 2002-05-06
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                                                                      Similarity
PDDRDFEPSLGPVCPFRCQCHLRVVQCSDLGLDKVPKDLPPDTTLLDLQNNKITEIKDGD 70
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Wood, William
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Gurney, Austin L.
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Gerritsen, Mary E.
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Filvaroff, Ellen
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b. US20030138885A1
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                                                       Conservative
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Pred. No. 5.4e-80;
60; Mismatches 82
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                                                     Score 943.5; DB 12
Pred. No. 5.4e-80;
0; Mismatches 82;
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TITLE OF INVENTION: SECRETED AND THANSMERGER.
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C167
CURRENT APPLICATION UMBER: US/10/140,021
CURRENT FILING DATE: 2002-05-66
PTIOT Application removed - See Palm or File
UMBER OF SEQ ID NOS: 550
SEQ ID NO 328
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TYPE: PRT
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US-10-140-021-328
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Best Local Similarity
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APPLICANT:
APPLICANT:
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PSLTELHLDGNKISRVDAASLKGLNNLAKLGLSFNSISAVDNGSLANTPHLRELHLDNNK 250
                          PRSHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKEND
                                                                                     FKNLKNLHALILVNNKISKVSPGAFTPLVKLERLYLSKNQLKELPEKMPKTLQELRAHEN 130
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
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Filvaroff, Ellen
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Search completed: February 9, 2004, 11:48:19
Job time: 81 secs